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OM protein - protein search, using sw model

Run on: May 11, 2004, 16:49:53 ; Search time 54 Seconds
(without alignments)
261.618 Million cell updates/sec

Title: us-10-006-252a-10
Perfect score: 301
Sequence: 1 KLCRSSGTWGVCGNNAC.....QHGSNCYVFAHKICVYPC 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep29Jan04:*
1: Genesep1980s:*
2: Genesep1990s:*
3: Genesep2000s:*
4: Genesep2001s:*
5: Genesep2002s:*
6: Genesep2003as:*
7: Genesep2003bs:*
8: Genesep2004s:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	301	100.0	50	2 AAW19282	Aaw19282 Raphanus
2	301	100.0	50	2 AAW40350	Aaw40350 Radish Rs
3	301	100.0	50	4 AAB49478	Aab49478 Radish an
4	294	97.7	50	2 AAW26384	Aaw26384 Radish an
5	294	97.7	50	2 AAW26382	Aaw26382 Radish an
6	293	97.3	50	2 AAW26381	Aaw26381 Radish an
7	292	97.0	50	2 AAW26385	Aaw26385 Radish an
8	286	95.0	50	2 AAW26383	Aaw26383 Radish an
9	282	93.7	51	2 AAW19283	Aaw19283 Raphanus
10	282	93.7	51	4 AAB49479	Aab49479 Radish an
11	281	93.4	51	2 AAW19281	Aaw19281 Raphanus
12	281	93.4	51	2 AAW19616	Aaw19616 Radish an
13	281	93.4	51	2 AAY00737	Aay00737 Antifunga
14	281	93.4	51	4 AAB67416	Aab67416 Amino aci
15	281	93.4	51	4 AAB20221	Aab20221 Radish de
16	281	93.4	51	4 AAB49471	Aab49471 Radish an
17	281	93.4	80	2 AAR33708	Aar33708 Antifunga
18	281	93.4	80	2 AAR57327	Aar57327 Antimicro
19	281	93.4	80	3 AAY91117	Aay91117 Raphanus
20	281	93.4	80	4 AAB61792	Aab61792 Radish an
21	281	93.4	149	3 AAY70323	Aay70323 Dahlia me
22	281	93.4	149	3 AAY84058	Aay84058 Amino aci
23	281	93.4	149	3 AAY84056	Aay84056 Amino aci
24	281	93.4	173	3 AAY84059	Aay84059 Amino aci
25	279	92.7	50	4 AAE10625	Aae10625 Radish pl

26	279	92.7	51	2 AAW40349	Aaw40349 Radish Rs
27	279	92.7	51	2 AAY00738	Aay00738 Antifunga
28	279	92.7	51	4 AAB67417	Aab67417 Amino aci
29	279	92.7	51	4 AAB20220	Aab20220 Radish de
30	279	92.7	51	4 AAB49470	Aab49470 Radish an
31	279	92.7	51	4 AAB61793	Aab61793 White mus
32	279	92.7	80	2 AAR33706	Aar33706 Antifunga
33	279	92.7	80	2 AAR57325	Aar57325 Antimicro
34	279	92.7	80	2 AAW19280	Aaw19280 Raphanus
35	279	92.7	80	2 AAW19617	Aaw19617 Radish an
36	279	92.7	80	5 AAY57564	Aay57564 Wasabia j
37	279	92.7	80	5 ABP53725	Abp53725 Wasabia j
38	279	92.7	80	7 ADC51222	Adc51222 Brassica
39	279	92.7	80	7 ADC51224	Adc51224 Brassica
40	277	92.0	51	2 AAW26379	Aaw26379 Radish an
41	276	91.7	51	2 AAW26387	Aaw26387 Antifunga
42	275	91.4	51	2 AAW26389	Aaw26389 Antifunga
43	274	91.0	51	2 AAW26386	Aaw26386 Antifunga
44	274	91.0	51	2 AAW26377	Aaw26377 Radish an
45	274	91.0	51	2 AAW40347	Aaw40347 A. thalia

ALIGNMENTS

RESULT 1
AAW19282
ID AAW19282 standard; protein; 50 AA.
XX AC AAW19282;
XX
DT 25-MAR-2003 (revised)
DT 21-JAN-1998 (first entry)
XX
DE Raphanus sativus antifungal protein 3 (RS-APP3).
XX
KW Antifungal protein; candida; fungal resistance; food additive; radish;
KW crop protection; plant defensin; bacterial protection; preservative.
XX
OS Raphanus sativus.
XX
FN WO9721815-A2.
XX
PD 19-JUN-1997.
XX
PF 12-DEC-1996; 96WO-GB003068.
XX
PR 13-DEC-1995; 95GB-00025455.
PR 28-MAR-1996; 96GB-00006552.
(ZENE) ZENECA LTD.
Meloan RH, Puijk WC, Schaaper WM, Sijtsma L, Van Amerongen A;
Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;
Van Gelder WMJ;
WPI; 1997-332786/30.
Antifungal peptide derived from radish antifungal protein 2 - and related
DNA, useful for producing plants with increased fungal resistance and as
therapeutic or preservative agent.
Disclosure; Fig 1; 65pp; English.

App. parent doc

This protein sequence is the Raphanus sativus (radish) mature antifungal protein (RS-APP3), which is homologous to proteins AAW19280- AAW19290. Shorter peptides, based on these proteins have been produced (see AAW19291-92, AAW19294-98, AAW19301-304, AAW19330-34 and AAW1765-834). Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease resistance or disease

CC tolerance of crops, either pre or post harvest. When applied to plants
 CC they may also have curative as well as protective actions. The peptides
 CC may also be used to protect plants by introducing them, or a
 CC microorganism capable of expressing the peptide into the soil. (Updated
 CC on 25-MAR-2003 to correct PI field.)
 XX
 XX

SQ Sequence 50 AA;

Query Match 100.0%; Score 301; DB 2; Length 50;
 Best Local Similarity 100.0%; Pred. No. 6.3e-25;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLCERSGTSWGVCGNNACKNQIRLEGAQHSGSNVYVFAHKICVYPC 50
 |||||
 DB 1 KLCERSGTSWGVCGNNACKNQIRLEGAQHSGSNVYVFAHKICVYPC 50

RESULT 2

AAW40350 ID AAW40350 standard; protein; 50 AA.

XX AC AAW40350;

XX DT 23-JUN-1998 (first entry)

XX DE Radish Rs-APP3 mature protein domain.

XX KW Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;
 XX fungus; radish.

XX OS Raphanus sativus.

XX FN WO9800023-A2.

XX PD 08-JAN-1998.

XX PF 20-JUN-1997; 97WO-GB001672.

XX PR 01-JUL-1996; 96GB-00013753.

XX PA (ZONE) ZENECA LTD.

XX PI Broekaert WF, Thomma BPHJ, Penninx IMA, Terras PRG, Manners JM;

XX FI Kazan K;

XX DR WPI; 1998-086663/08.

XX PT Protecting plants against pathogens by inducing defensin genes - by
 XX stimulating ethylene or jasmonate pathways, also new promoter of defensin
 XX gene from Arabidopsis.

XX PS Disclosure; Fig 1C; 72pp; English.

XX CC This sequence represents the radish Rs-APP3 mature protein domain which
 CC is used to explain a novel method for the protection of plants against
 CC pathogens which involves inducing expression of a plant defensin gene by
 CC stimulating the jasmonate and/or ethylene pathways. The method is used to
 CC induce protection against necrotrophic pathogens, specifically fungi and
 CC does not require cytotoxic or potentially harmful chemicals

XX SQ Sequence 50 AA;

Query Match 100.0%; Score 301; DB 2; Length 50;
 Best Local Similarity 100.0%; Pred. No. 6.3e-25;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLCERSGTSWGVCGNNACKNQIRLEGAQHSGSNVYVFAHKICVYPC 50
 |||||
 DB 1 KLCERSGTSWGVCGNNACKNQIRLEGAQHSGSNVYVFAHKICVYPC 50

RESULT 3

AAW49478

ID AAB49478 standard; protein; 50 AA.

XX AC AAB49478;

XX DT 07-MAR-2001 (first entry)

XX DE Radish antifungal protein Rs-APP3.

XX KW Radish; antifungal; antimicrobial.

XX OS Raphanus sativus.

XX FN WO200071735-A1.

XX PD 30-NOV-2000.

XX PF 18-MAY-2000; 2000WO-GB001905.

XX PR 21-MAY-1999; 99GB-00011933.

XX PA (ZONE) ZENECA LTD.

XX PI Greenland AJ, Fuentes Mateos AM;

XX DR WPI; 2001-041066/05.

XX PT Antimicrobial composition useful for treating microbial diseases in
 XX plants, comprises two antimicrobial agents, which are antifungal protein
 XX from Radish and Mirabilis of Impatiens.

XX PS Disclosure; Page 26; 29pp; English.

XX CC The present sequence is an antifungal protein from Radish. This protein
 CC is useful for treating microbial diseases in plants and for inhibiting
 CC microbial growth in foodstuffs. In addition, the present sequence is
 CC useful for producing plants with improved resistance to microbial
 CC pathogens. The present protein can be used in conjunction with other
 CC antimicrobial proteins from Mirabilis (see AAB49472-B49473), and
 XX Impatiens (see AAB49474-B49477) to form an antimicrobial composition

XX SQ Sequence 50 AA;

Query Match 100.0%; Score 301; DB 4; Length 50;

Best Local Similarity 100.0%; Pred. No. 6.3e-25;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLCERSGTSWGVCGNNACKNQIRLEGAQHSGSNVYVFAHKICVYPC 50
 |||||

DB 1 KLCERSGTSWGVCGNNACKNQIRLEGAQHSGSNVYVFAHKICVYPC 50
 |||||

RESULT 4

AAW26384

ID AAW26384 standard; protein; 50 AA.

XX AC AAW26384;

XX DT 13-DEC-1997 (first entry)

XX DE Radish antifungal protein 2 mutant (delQ1.Q5M/P7S/K30G).

XX KW Rs-APP2; radish antifungal protein 2; fungicide; salt tolerance;
 XX preservative; transgenic plant; crop protection.

XX OS Raphanus; sativus.

XX OS Synthetic.

XX OS Chimeric.

XX PN WO9721814-A1.

XX PD 19-JUN-1997.

XX PF 12-DEC-1996; 96WO-GB003065.

*App. 1, 2007
 doc.*

XX 13-DEC-1995; 95GB-00025474.
 XX (ZENE) ZENECA LTD.
 XX Broekaert WF, De Samblanx GW, Rees SB;
 XX WPI; 1997-332785/30.
 XX New active mutants of radish antifungal protein 2 - used to generate
 PT fungus-resistant plants or as therapeutic or preservative agents.
 PT Disclosure; Page 4; 39pp; English.
 XX This polypeptide comprises a mutant isoform of radish antifungal protein
 CC 2 (Rs-APP2) (see also AAW19616). Novel potent antifungal proteins (see
 CC AAW26371-90) are based on Rs-APP2 and contain at least 1 mutation
 CC selected from a basic residue at positions 9 or 39, and a hydrophobic
 CC residue at positions 5 or 16. Proteins containing Glu5Met (see AAW26379),
 CC Gly16Met (AAW26380), Gly9Arg (AAW26376), Val39Arg (AAW26377) or Gly9Arg
 CC plus Val39Arg (AAW26378) mutations are specifically claimed. A cDNA clone
 CC encoding Rs-APP2 preprotein can be modified by recombinant DNA methods to
 CC allow expression of mutant isoforms in yeast as mating factor alpha 1
 CC fusion proteins. The Rs-APP2 mutants have enhanced salt tolerant
 CC antifungal activity, especially when expressed in plant tissue where that
 CC may have curative as well as protective effects. They are useful for
 CC combating fungal diseases in agricultural, pharmaceutical or preservative
 CC applications
 XX Sequence 50 AA;
 SQ Query Match 97.7%; Score 294; DB 2; Length 50;
 Best Local Similarity 98.0%; Pred. No. 3.5e-24;
 Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLCRSSGTWSGVCNNACKNQICIRLEGAGHGSNCYVFPFAHKICICYPPC 50
 |||||
 DB 1 KLCMRSSGTWSGVCNNACKNQICIRLEGAGHGSNCYVFPFAHKICICYPPC 50
 |||||

RESULT 5
 AAW26382
 ID AAW26382 standard; protein; 50 AA.
 AC AAW26382;
 XX 13-DEC-1997 (first entry)
 DE Radish antifungal protein 2 mutant (delQ1,Q5E/P7S/K30G/V39R).
 XX Rs-APP2; radish antifungal protein 2; fungicide; salt tolerance;
 KW preservative; transgenic plant; crop protection.
 XX Raphanus; sativus.
 OS Synthetic.
 OS Chimeric.
 XX WO9721814-A1.
 XX 19-JUN-1997.
 XX 12-DEC-1996; 96WO-GB003065.
 XX 13-DEC-1995; 95GB-00025474.
 XX (ZENE) ZENECA LTD.
 XX Broekaert WF, De Samblanx GW, Rees SB;
 XX WPI; 1997-332785/30.
 XX New active mutants of radish antifungal protein 2 - used to generate
 PT fungus-resistant plants or as therapeutic or preservative agents.

XX Disclosure; Page 4; 39pp; English.
 XX This polypeptide comprises a mutant isoform of radish antifungal protein
 CC 2 (Rs-APP2) (see also AAW19616). Novel potent antifungal proteins (see
 CC AAW26371-90) are based on Rs-APP2 and contain at least 1 mutation
 CC selected from a basic residue at positions 9 or 39, and a hydrophobic
 CC residue at positions 5 or 16. Proteins containing Glu5Met (see AAW26379),
 CC Gly16Met (AAW26380), Gly9Arg (AAW26376), Val39Arg (AAW26377) or Gly9Arg
 CC plus Val39Arg (AAW26378) mutations are specifically claimed. A cDNA clone
 CC encoding Rs-APP2 preprotein can be modified by recombinant DNA methods to
 CC allow expression of mutant isoforms in yeast as mating factor alpha 1
 CC fusion proteins. The Rs-APP2 mutants have enhanced salt tolerant
 CC antifungal activity, especially when expressed in plant tissue where that
 CC may have curative as well as protective effects. They are useful for
 CC combating fungal diseases in agricultural, pharmaceutical or preservative
 CC applications
 XX Sequence 50 AA;
 SQ Query Match 97.7%; Score 294; DB 2; Length 50;
 Best Local Similarity 98.0%; Pred. No. 3.5e-24;
 Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLCRSSGTWSGVCNNACKNQICIRLEGAGHGSNCYVFPFAHKICICYPPC 50
 |||||
 DB 1 KLCMRSSGTWSGVCNNACKNQICIRLEGAGHGSNCYVFPFAHKICICYPPC 50
 |||||

RESULT 6
 AAW26381
 ID AAW26381 standard; protein; 50 AA.
 AC AAW26381;
 XX 13-DEC-1997 (first entry)
 DE Radish antifungal protein 2 mutant (delQ1,Q5E/P7S/G9R/K30G).
 XX Rs-APP2; radish antifungal protein 2; fungicide; salt tolerance;
 KW preservative; transgenic plant; crop protection.
 XX Raphanus; sativus.
 OS Synthetic.
 OS Chimeric.
 XX WO9721814-A1.
 XX 19-JUN-1997.
 XX 12-DEC-1996; 96WO-GB003065.
 XX 13-DEC-1995; 95GB-00025474.
 XX (ZENE) ZENECA LTD.
 XX Broekaert WF, De Samblanx GW, Rees SB;
 XX WPI; 1997-332785/30.
 XX New active mutants of radish antifungal protein 2 - used to generate
 PT fungus-resistant plants or as therapeutic or preservative agents.
 PT Disclosure; Page 4; 39pp; English.

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CC allow expression of mutant isoforms in yeast as mating factor alpha 1
 CC fusion proteins. The Rs-AFP2 mutants have enhanced salt tolerant
 CC antifungal activity, especially when expressed in plant tissue where that
 CC may have curative as well as protective effects. They are useful for
 CC combating fungal diseases in agricultural, pharmaceutical or preservative
 CC applications
 XX
 SQ Sequence 50 AA;

Query Match 97.3%; Score 293; DB 2; Length 50;
 Best Local Similarity 98.0%; Pred. No. 4.5e-24;
 Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KLCERSSTWVGCGNNACKNQICIRLEGAHGSCNYYVFFPAHKICICYFPC 50
 |||||
 DB 1 KLCERSSTWVGCGNNACKNQICIRLEGAHGSCNYYVFFPAHKICICYFPC 50
 |||||

RESULT 7
 AAW26385
 ID AAW26385 standard; protein; 50 AA.
 XX
 AC AAW26385;
 XX
 DT 13-DEC-1997 (first entry)
 XX

DE Radish antifungal protein 2 mutant (delQ1,Q5E/P7S/G16W/K30G).
 XX
 KW Rs-AFP2; radish antifungal protein 2; fungicide; salt tolerance;
 KW preservative; transgenic plant; crop protection.
 XX

OS Raphanus; sativus.
 OS Synthetic.
 OS Chimeric.
 XX
 PN WO9721814-A1.
 XX
 PD 19-JUN-1997.
 XX

PF 12-DEC-1996; 96WO-GB003065.
 XX
 PR 13-DEC-1995; 95GB-00025474.
 XX

PA (ZENE) ZENECA LTD.
 XX
 PI Broekaert WF, De Samblanx GW, Rees SB;
 XX
 DR WPI; 1997-332785/30.
 XX

PT New active mutants of radish antifungal protein 2 - used to generate
 PT fungus-resistant plants or as therapeutic or preservative agents.
 XX
 PS Disclosure; Page 4; 39pp; English.
 XX

CC This polypeptide comprises a mutant isoform of radish antifungal protein
 CC 2 (Rs-AFP2) (see also AAW19616). Novel potent antifungal proteins (see
 CC AAW26371-90) are based on Rs-AFP2 and contain at least 1 mutation
 CC selected from a basic residue at positions 9 or 39, and a hydrophobic
 CC residue at positions 5 or 16. Proteins containing Gln5Met (see AAW26379),
 CC Gly16Met (AAW26380), Gly9Arg (AAW26376), Val39Arg (AAW26377) or Gly9Arg
 CC plus Val39Arg (AAW26378) mutations are specifically claimed. A cDNA clone
 CC encoding Rs-AFP2 preprotein can be modified by recombinant DNA methods to
 CC allow expression of mutant isoforms in yeast as mating factor alpha 1
 CC fusion proteins. The Rs-AFP2 mutants have enhanced salt tolerant
 CC antifungal activity, especially when expressed in plant tissue where that
 CC may have curative as well as protective effects. They are useful for
 CC combating fungal diseases in agricultural, pharmaceutical or preservative
 CC applications
 XX

Query Match 97.0%; Score 292; DB 2; Length 50;
 Best Local Similarity 98.0%; Pred. No. 5.7e-24;

Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 KLCERSSTWVGCGNNACKNQICIRLEGAHGSCNYYVFFPAHKICICYFPC 50
 |||||
 DB 1 KLCERSSTWVGCGNNACKNQICIRLEGAHGSCNYYVFFPAHKICICYFPC 50
 |||||

RESULT 8
 AAW26383
 ID AAW26383 standard; protein; 50 AA.
 XX
 AC AAW26383;
 XX

DT 13-DEC-1997 (first entry)
 XX
 DE Radish antifungal protein 2 mutant (delQ1,Q5E/P7S/G9R/K30G/V39R).
 XX

KW Rs-AFP2; radish antifungal protein 2; fungicide; salt tolerance;
 KW preservative; transgenic plant; crop protection.
 XX

OS Raphanus; sativus.
 OS Synthetic.
 OS Chimeric.
 XX

PN WO9721814-A1.
 XX
 PD 19-JUN-1997.
 XX

PF 12-DEC-1996; 96WO-GB003065.
 XX
 PR 13-DEC-1995; 95GB-00025474.
 XX

PA (ZENE) ZENECA LTD.
 XX
 PI Broekaert WF, De Samblanx GW, Rees SB;
 XX
 DR WPI; 1997-332785/30.
 XX

PT New active mutants of radish antifungal protein 2 - used to generate
 PT fungus-resistant plants or as therapeutic or preservative agents.
 XX
 PS Disclosure; Page 4; 39pp; English.
 XX

CC This polypeptide comprises a mutant isoform of radish antifungal protein
 CC 2 (Rs-AFP2) (see also AAW19616). Novel potent antifungal proteins (see
 CC AAW26371-90) are based on Rs-AFP2 and contain at least 1 mutation
 CC selected from a basic residue at positions 9 or 39, and a hydrophobic
 CC residue at positions 5 or 16. Proteins containing Gln5Met (see AAW26379),
 CC Gly16Met (AAW26380), Gly9Arg (AAW26376), Val39Arg (AAW26377) or Gly9Arg
 CC plus Val39Arg (AAW26378) mutations are specifically claimed. A cDNA clone
 CC encoding Rs-AFP2 preprotein can be modified by recombinant DNA methods to
 CC allow expression of mutant isoforms in yeast as mating factor alpha 1
 CC fusion proteins. The Rs-AFP2 mutants have enhanced salt tolerant
 CC antifungal activity, especially when expressed in plant tissue where that
 CC may have curative as well as protective effects. They are useful for
 CC combating fungal diseases in agricultural, pharmaceutical or preservative
 CC applications
 XX

SQ Sequence 50 AA;

Query Match 95.0%; Score 286; DB 2; Length 50;
 Best Local Similarity 96.0%; Pred. No. 2.5e-23;
 Matches 48; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 KLCERSSTWVGCGNNACKNQICIRLEGAHGSCNYYVFFPAHKICICYFPC 50
 |||||
 DB 1 KLCERSSTWVGCGNNACKNQICIRLEGAHGSCNYYVFFPAHKICICYFPC 50
 |||||

RESULT 9
 AAW19283
 ID AAW19283 standard; protein; 51 AA.
 XX


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AC AAW19283;
XX
XX 25-MAR-2003 (revised)
DT 21-JAN-1998 (first entry)
XX
XX Raphanus sativus antifungal protein 4 (Rs-APP4).
DE
XX Antifungal protein; candida; fungal resistance; food additive; radish;
XX crop protection; plant defensin; bacterial protection; preservative.
KW
XX Raphanus sativus.
XX
XX WO9721815-A2.
XX
XX 19-JUN-1997.
XX
XX 12-DEC-1996; 96WO-GB003068.
XX
XX 13-DEC-1995; 95GB-00025455.
XX
XX 28-MAR-1996; 96GB-00006552.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Meloen RH, Puijk WC, Schaaper WMW, Sijtsma L, Van Amerongen A;
XX Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB,
XX Van Gelder WMJ;
XX
XX WPI; 1997-332786/30.
XX
XX Antifungal peptide derived from radish antifungal protein 2 - and related
XX DNA, useful for producing plants with increased fungal resistance and as
XX therapeutic or preservative agent.
XX
XX Disclosure; Fig 1; 65pp; English.
XX
XX This protein sequence is the Raphanus sativus (radish) mature antifungal
XX protein (Rs-APP4), which is homologous to proteins AAW19280- AAW19290.
XX Shorter peptides, based on these proteins have been produced (see
XX AAW19291-92, AAW19294-98, AAW19301-304, AAW19330-34 and AAW1765-834).
XX Plants containing DNA sequences encoding these proteins have improved
XX resistance to fungi. Compositions containing the peptides can be used to
XX control fungi or bacteria in pharmaceutical (e.g. treatment of Candida
XX infections) or preservative purposes (as food additives). In agriculture,
XX the peptide may be used to improve disease resistance or disease
XX tolerance of crops, either pre or post harvest. When applied to plants
XX they may also have curative as well as protective actions. The peptides
XX may also be used to protect plants by introducing them, or a
XX microorganism capable of expressing the peptide into the soil. (Updated
XX on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 51 AA;

Query Match 93.7%; Score 282; DB 2; Length 51;
Best Local Similarity 90.0%; Pred. No. 6.7e-23;
Matches 45; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCRSSGTWVGCGNNACKNQCRLEGAGHGSNCYVFPAAHKICYPFC 50
Db 2 KLCRSSGTWVGCGNNACKNQCNINLEGARHGSNCYIFPHRCICYPFC 51

RESULT 10
AAW19281
ID AAW19281 standard; protein; 51 AA.
XX
XX AAW19281;
AC
XX 25-MAR-2003 (revised)
DT 21-JAN-1998 (first entry)
XX
XX Raphanus sativus antifungal protein 2 (Rs-APP2).
DE
XX Antifungal protein; candida; fungal resistance; food additive; radish;
XX crop protection; plant defensin; bacterial protection; preservative.
KW
XX Raphanus sativus.
XX
XX WO9721815-A2.
XX
XX 19-JUN-1997.
XX
XX 12-DEC-1996; 96WO-GB003068.
XX
XX 13-DEC-1995; 95GB-00025455.
XX
XX 28-MAR-1996; 96GB-00006552.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Meloen RH, Puijk WC, Schaaper WMW, Sijtsma L, Van Amerongen A;
XX Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;
XX Van Gelder WMJ;
XX
XX WPI; 1997-332786/30.
XX
```

XX Antifungal peptide derived from radish antifungal protein 2 - and related
PT DNA, useful for producing plants with increased fungal resistance and as
PT therapeutic or preservative agent.
XX
PS Disclosure; Fig 1; 65pp; English.
XX
XX This protein sequence is the Rhanus sativus (radish) mature antifungal
CC protein (Rs-APP2), which is homologous to proteins AAW19280- AAW19290.
CC Shorter peptides, based on these proteins have been produced (see
CC AAW19291-92, AAW19294-98, AAW19301-304, AAW19330-34 and AAW31765-834).
CC Plants containing DNA sequences encoding these proteins have improved
CC resistance to fungi. Compositions containing the peptides can be used to
CC control fungi or bacteria in pharmaceutical (e.g. treatment of Candida
CC infections) or preservative purposes (as food additives). In agriculture,
CC the peptide may be used to improve disease resistance or disease
CC tolerance of crops, either pre or post harvest. When applied to plants
CC they may also have curative as well as protective actions. The peptides
CC may also be used to protect plants by introducing them, or a
CC microorganism capable of expressing the peptide into the soil. (Updated
CC on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 51 AA;

Query Match 93.4%; Score 281; DB 2; Length 51;
Best Local Similarity 92.0%; Pred. No. 8.6e-23;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KLCERSSTGWSGVCNNACNQCIRLEGAHQSCNYYVFPFAHKICVYFPC 50
DB 2 KLCQSPSTGWSGVCNNACNQCIRLEKARHGSCNYYVFPFAHKICVYFPC 51

RESULT 12
AAW19616
ID AAW19616 standard; protein; 51 AA.
XX
AC AAW19616;
XX
DT 13-DEC-1997 (first entry)
XX
DE Radish antifungal protein 2 (Rs-APP2).
XX
KW Rs-APP2; radish antifungal protein 2; fungicide; salt tolerance;
KW preservative; transgenic plant; crop protection.
XX
OS Raphanus sativus.
XX
FH Key Location/Qualifiers
FT Misc-difference 5 /note= "Gln at position 5 may be replaced by a
FT hydrophobic amino acid, preferably Met"
FT Misc-difference 9 /note= "Gly at position 9 may be replaced by a basic
FT amino acid, preferably Arg"
FT Misc-difference 16 /note= "Gly at position 16 may be replaced by a
FT hydrophobic amino acid, preferably Met"
FT Misc-difference 39 /note= "Val at position 39 may be replaced by a basic
FT amino acid, preferably Arg"
XX
PN WO9721814-A1.
XX
XX 19-JUN-1997.
PD
XX 12-DEC-1996; 96WO-GB003065.
XX
PR 13-DEC-1995; 95GB-00025474.
XX
XX (ZENE) ZENECA LTD.
PA
PI Broekaert WF, De Samblanx GW, Rees SB;

XX WPI; 1997-332785/30.
DR
XX New active mutants of radish antifungal protein 2 - used to generate
PT fungus-resistant plants or as therapeutic or preservative agents.
XX
XX Claim 1; Fig 1; 39pp; English.
XX
XX This polypeptide comprises radish antifungal protein 2 (Rs-APP2). Novel
CC potent antifungal proteins (see AAW26371-90) based on Rs-APP2 contain at
CC least 1 mutation selected from a basic residue at positions 9 or 39, and
CC a hydrophobic residue at positions 5 or 16. Proteins containing Gln5Met
CC (see AAW26379), Gly16Met (AAW26380), Gly9Arg (AAW26376), Val39Arg
CC (AAW26377) or Gly9Arg plus Val39Arg (AAW26378) mutations are specifically
CC claimed. A cDNA clone encoding Rs-APP2 preprotein can be modified by
CC recombinant DNA methods to allow expression of mutant isoforms in yeast
CC as mating factor alpha 1 fusion proteins. The Rs-APP2 mutants have
CC enhanced salt tolerant antifungal activity, especially when expressed in
CC plant tissue where that may have curative as well as protective effects.
CC They are useful for combating fungal diseases in agricultural,
CC pharmaceutical or preservative applications
XX
SQ Sequence 51 AA;

Query Match 93.4%; Score 281; DB 2; Length 51;
Best Local Similarity 92.0%; Pred. No. 8.6e-23;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 KLCERSSTGWSGVCNNACNQCIRLEGAHQSCNYYVFPFAHKICVYFPC 50
DB 2 KLCQSPSTGWSGVCNNACNQCIRLEKARHGSCNYYVFPFAHKICVYFPC 51

RESULT 13
AAW00737
ID AAY00737 standard; peptide; 51 AA.
XX
AC AAY00737;
XX
DT 14-MAY-1999 (first entry)
XX
DE Antifungal peptide RsAPP2.
XX
KW Antifungal agent; food additive; food spoilage prevention.
XX
OS Synthetic.
XX
PN WO9902038-A1.
XX
XX 21-JAN-1999.
PD
XX 09-JUL-1998; 98WO-GB002010.
PF
XX 10-JUL-1997; 97GB-00014564.
PR (ZENE) ZENECA LTD.
XX
XX Greenland AJ, Fuentes Mateos AM;
PI
XX WPI; 1999-120402/10.
DR
XX Food additive synergistically enhances activity of an antifungal agent -
PT especially for prevent food and beverage spoilage.
XX
XX Claim 15; Fig 7; 40pp; English.
XX
XX This sequence represents an antifungal peptide. The invention relates to
CC an antifungal composition comprising one or more antifungal agents and
CC one or more food additives, providing that the composition does not
CC contain nicin or lactoferrin or a derivative, trichorizamine or lysozyme,
CC the relative amounts of antifungal agent and food additive being such
CC that they enhance the activity of the overall antifungal activity of the
CC composition. Especially the antifungal agent is derived from a plant or

CC seed and the food additive is selected from an acid, salt or ester or a 1
 CC -6C alkyl ether or derivatives. The compositions are useful in preventing
 CC food spoilage e.g. in a wide range of foods and beverages including
 CC fruits, jams and dairy products, caused by the spoilage organisms
 CC *Fusarium culmorum*, *Penicillium chrysogenum*, *P. roquefortii*, *P.*
 CC *naligovense*, *P. commune*, *Alternaria* sp., *Cladosporium* sp., *Tichodermma*
 CC *harzianum*, *Mucor plumbeus*, *Aspergillus versicolor* and *Scopulariopsis*
 CC *brevicaulis*. The food additive and antifungal agent act synergistically
 CC to enhance the overall antifungal activity of the composition to a level
 CC above the sum of each single component
 XX
 XX SQ Sequence 51 AA;

Query Match 93.4%; Score 281; DB 2; Length 51;
 Best Local Similarity 92.0%; Pred. No. 8.6e-23;
 Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCRSSGTWSGVCNNACKQCIRLEGAQHGSNCNVFPAHKCICYPPC 50
 ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 2 KLCQPSGTWSGVCNNACKQCIRLEKARHGSCNVFPAHKCICYPPC 51

RESULT 14

AAB67416
 ID AAB67416 standard; protein; 51 AA.

XX AAB67416;

DT 15-MAY-2001 (first entry)

XX Amino acid sequence of the plant defensin Rs-APP2.

XX Defensin; antimicrobial; microbial infection; fungal infection;
 XX pathogenic fungi; bacterial infection; transgenic plant;
 XX microbial pathogen; fungal resistance.

XX *Raphanus sativus*.

PN WO200109175-A2.

PD 08-FEB-2001.

PF 31-JUL-2000; 2000WO-GB002968.

PR 02-AUG-1999; 99GB-00018156.

XX (ZENE-) ZENECA LTD.

XX Posthuma GA, Schaaper WM, Sijtsma L, Van Amerongen A, Fant F;
 PI Borremans FAM, Rees SB, Osborn RW;

XX WPI; 2001-182939/18.

XX Antimicrobial peptide for combating bacterial infections, comprises
 PT modified cysteine residues, modified by addition, substitution or
 PT deletion to block their ability to form disulfide bridges.

XX Disclosure; Page 3; 45pp; English.

XX The present sequence represents a plant defensin protein. Defensins
 CC have antimicrobial properties. The specification describes a modified Cys
 CC -containing antimicrobial peptide derived from a plant defensin. The
 CC peptide is modified by introducing one or more Cys residues and/or
 CC replacing or altering one or more Cys residues to block their ability to
 CC form disulfide bridges. The antimicrobial peptide is useful in the
 CC treatment and prevention of microbial infections e.g. for combating
 CC fungal infection. It is useful for agricultural and pharmaceutical
 CC applications. It is also useful against a broad spectrum of pathogenic
 CC fungi and is also useful in combating bacterial infections. A DNA
 CC sequence encoding the antimicrobial peptide is useful for producing
 CC transgenic plants with increased resistance to microbial pathogen, such
 CC that the plant is used as a parent in standard plant breeding crosses to
 CC develop hybrids and lines having improved fungal resistance

XX SQ Sequence 51 AA;

Query Match 93.4%; Score 281; DB 4; Length 51;
 Best Local Similarity 92.0%; Pred. No. 8.6e-23;
 Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCRSSGTWSGVCNNACKQCIRLEGAQHGSNCNVFPAHKCICYPPC 50
 ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 2 KLCQPSGTWSGVCNNACKQCIRLEKARHGSCNVFPAHKCICYPPC 51

RESULT 15

AAB20221
 ID AAB20221 standard; protein; 51 AA.

XX AAB20221;

DT 14-MAY-2001 (first entry)

XX Radish defensin Rs-APP2.

XX Radish; defensin; Rs-APP2; antimicrobial; antifungal; fungicide;
 XX transgenic plant; disease resistance; infection; therapy.

XX *Raphanus sativus*.

XX Key Location/Qualifiers

FT Disulfide-bond 4..51

FT Disulfide-bond 15..36

FT Disulfide-bond 21..45

FT Disulfide-bond 25..47

FT Misc-difference 32

FT /note= "optionally substituted by Trp in antimicrobial

FT protein/peptide of Claim 1"

FT Misc-difference 34

FT /note= "optionally substituted by Val, Leu, Ile, Trp,

FT Phe, Lys, Arg, Tyr, Met, Cys or His in antimicrobial

FT protein/peptide of Claim 1"

FT Misc-difference 35

FT /note= "optionally substituted by Ile, Trp, Lys, Arg,

FT Val, Leu, Phe, His in antimicrobial protein/peptide of

FT Claim 1"

FT Misc-difference 36

FT /note= "optionally substituted by Trp in antimicrobial

FT protein/peptide of Claim 1"

FT Misc-difference 37

FT /note= "optionally substituted by Trp, Gly, Thr, Tyr,

FT Gln, Lys, Arg, Phe or His in antimicrobial

FT protein/peptide of Claim 1"

FT Misc-difference 38

FT /note= "optionally substituted by Leu, Ile, Trp, Phe,

FT Val, Cys in antimicrobial protein/peptide of Claim 1"

FT Misc-difference 39

FT /note= "optionally substituted by Leu, Ile, Trp, Phe,

FT Met, Lys, Arg, Tyr or His in antimicrobial

FT protein/peptide of Claim 1"

FT Misc-difference 40

FT /note= "optionally substituted by Trp in antimicrobial

FT protein/peptide of Claim 1"

FT Misc-difference 41

FT /note= "optionally substituted by Ile, Trp, Phe, Ser,

FT Thr, Tyr, Gln, Asn, Lys, Arg or His in antimicrobial

FT protein/peptide of Claim 1"

FT Misc-difference 42

FT /note= "optionally substituted by Val, Leu, Ile, Trp,

FT Phe, Tyr, Asn, Lys, Arg, Ser or Thr in antimicrobial

FT protein/peptide of Claim 1"

PN WO200109174-A2.

PD 08-FEB-2001.

XX

```

31-JUL-2000; 200OWO-GB002941.
02-AUG-1999; 99GB-00018155.
(ZENE ) ZENECA LTD.
Posthuma GA, Schaaper WWM, Sijtsma L, Van Amerongen A, Fant F;
Borremans FAM;
WPI; 2001-182938/18.
Novel antimicrobial proteins derived from plant defensin useful against a
broad spectrum of microbes, comprise substitutions at specified portions
of its sequence.
Disclosure; Page 6; 64pp; English.
The present sequence is that of radish defensin protein Rs-APP2. A
claimed antimicrobial protein or peptide is derived from a plant defensin
characterised by having 1 or more replacement amino acids, as indicated
at positions 32, 34, 35, 36, 37, 38, 39, 40, 41 and/or 42 of the Rs-APP2
sequence, provided that the replacement amino acids are not found
naturally at these positions and the protein does not comprise only a
replacement arginine at position 37, 39 or 42. In addition, cysteine
residues may be replaced by alpha-aminobutyric acid. The antimicrobial
protein or peptide is preferably derived from RS-APF1 (see AAB20220), RS-
APF1, RS-APP3, RS-APP4, Br-APF1, Br-APP2, Bn-APF1, Bn-APP2, Sa-APF1, Sa-
APP2, Aa-APF1, Rs-APP2, Ah-AMP1 or Dm-AMP1. The antimicrobial protein or
peptide can be used on its own, or in synergistic combination with a
plant defensin, to combat fungi. A plant having improved resistance to a
fungal or microbial pathogen can contain recombinant DNA which expresses
a claimed antimicrobial protein or peptide. The claimed antimicrobial
protein or peptide is also used as a pharmaceutical to treat or prevent a
microbial infection, especially a fungal infection (all claimed)
Sequence 51 AA;
Query Watch          93.4%; Score 281; DB 4; Length 51;
Best Local Similarity 92.0%; Pred. No. 8.6e-23;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0
QY 1 KLCRSSGTSGVCGNNACNQCIRLEGAQHGSCTNYVFFAHKICVFFC 50
Db 2 KLCRPSGTSGVCGNNACNQCIRLEKARHGSCTNYVFFAHKICVFFC 51

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Search completed: May 11, 2004, 16:56:27
Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 16:55:24 ; Search time 23 Seconds
(without alignments)
112.230 Million cell updates/sec

Title: US-10-006-252A-10

Perfect score: 301

Sequence: 1 KLCRSSGTGSGVCGNNAC.....QHGSNYVFAHKICFYPC 50

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2.6/prodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2.6/prodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2.6/prodata/2/iaa/5A_COMB.pep.*
- 4: /cgn2.6/prodata/2/iaa/5B_COMB.pep.*
- 5: /cgn2.6/prodata/2/iaa/5A_COMB.pep.*
- 6: /cgn2.6/prodata/2/iaa/5B_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	301	100.0	50	4	US-09-077-951-10
2	301	100.0	50	4	US-09-077-948A-36
3	294	97.7	50	4	US-09-077-951-68
4	294	97.7	50	4	US-09-077-951-70
5	293	97.3	50	4	US-09-077-951-67
6	292	97.0	50	4	US-09-077-951-71
7	286	95.0	50	4	US-09-077-951-69
8	282	93.7	51	4	US-09-077-951-11
9	282	93.7	51	4	US-09-077-948A-37
10	281	93.4	51	1	US-08-656-318A-4
11	281	93.4	51	1	US-08-627-706-19
12	281	93.4	51	2	US-08-956-459-4
13	281	93.4	51	3	US-09-103-489-19
14	281	93.4	51	4	US-09-077-951-9
15	281	93.4	51	4	US-09-077-951-20
16	281	93.4	51	4	US-09-077-951-37
17	281	93.4	51	4	US-09-077-951-77
18	281	93.4	51	4	US-09-077-948A-35
19	281	93.4	51	4	US-09-829-381D-19
20	281	93.4	80	1	US-08-377-687-59
21	281	93.4	80	2	US-08-777-193-59
22	281	93.4	80	3	US-08-971-983-59
23	281	93.4	80	4	US-09-589-733C-21
24	279	92.7	51	1	US-08-377-687-19
25	279	92.7	51	1	US-08-656-318A-3
26	279	92.7	51	1	US-08-627-706-18
27	279	92.7	51	2	US-08-777-192-19

28	279	92.7	51	2	US-08-956-459-3	Sequence 3, Appl
29	279	92.7	51	3	US-08-971-982-19	Sequence 19, Appl
30	279	92.7	51	3	US-09-103-489-18	Sequence 18, Appl
31	279	92.7	51	4	US-09-077-951-8	Sequence 8, Appl
32	279	92.7	51	4	US-09-077-948A-34	Sequence 34, Appl
33	279	92.7	51	4	US-09-829-381D-18	Sequence 18, Appl
34	279	92.7	51	4	US-09-589-733C-22	Sequence 22, Appl
35	279	92.7	80	1	US-08-377-687-49	Sequence 49, Appl
36	279	92.7	80	2	US-08-777-192-49	Sequence 22, Appl
37	279	92.7	80	3	US-08-971-982-49	Sequence 49, Appl
38	279	92.7	80	3	US-09-103-489-20	Sequence 20, Appl
39	279	92.7	80	4	US-09-829-381D-20	Sequence 20, Appl
40	277	92.0	51	4	US-09-077-951-22	Sequence 22, Appl
41	277	92.0	51	4	US-09-077-951-29	Sequence 29, Appl
42	277	92.0	51	4	US-09-077-951-65	Sequence 65, Appl
43	276	91.7	51	4	US-09-077-951-31	Sequence 31, Appl
44	276	91.7	51	4	US-09-077-951-39	Sequence 39, Appl
45	276	91.7	51	4	US-09-077-951-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-077-951-10
; Sequence 10, Application US/09077951
; Patent No. 6372888
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Geneveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: PPD50093
; CURRENT APPLICATION NUMBER: US/09/077,951
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: GB 9525474.4
; EARLIER FILING DATE: 1995-12-13
; EARLIER APPLICATION NUMBER: PCT/GB96/03065
; EARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-09-077-951-10

Query Match 100.0%; Score 301; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLCRSSGTGSGVCGNNACNQICIRLEGAHQGSCNYVFAHKICFYPC 50
Db 1 KLCRSSGTGSGVCGNNACNQICIRLEGAHQGSCNYVFAHKICFYPC 50

RESULT 2
US-09-077-948A-36
; Sequence 36, Application US/09077948A
; Patent No. 6605698
; GENERAL INFORMATION:
; APPLICANT: Van Amerongen, Aart
; APPLICANT: Fant, Franky
; APPLICANT: Borremans, Frans
; APPLICANT: De Samblanx, Geneveva
; APPLICANT: Sitjtsma, Iolke
; APPLICANT: Meloen, Robbert
; APPLICANT: Puijk, Wouter
; APPLICANT: Schaaper, Wilhelmus
; APPLICANT: Broekaert, Willem
; APPLICANT: Van Gelder, Wilhelmus
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins

priority due.

priority due.

; FILE REFERENCE: 109846-257 (SYN-035)
; CURRENT APPLICATION NUMBER: US/09/077,948A
; CURRENT FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: PCT/GB96/03068
; PRIOR FILING DATE: 1996-12-12
; PRIOR APPLICATION NUMBER: GB 9606552.9
; PRIOR FILING DATE: 1996-03-28
; PRIOR APPLICATION NUMBER: GB 9525455.3
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-09-077-948A-36

Query Match 100.0%; Score 301; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 6.5e-26; Indels 0; Gaps 0;
Matches 50; Conservative 0; Mismatches 0;

QY 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50
|||
DB 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50
|||

RESULT 3

US-09-077-951-68
; Sequence 68, Application US/09077951
; Patent No. 6372888
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: PPD50093
; CURRENT APPLICATION NUMBER: US/09/077,951
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: GB 9525474.4
; EARLIER FILING DATE: 1995-12-13
; EARLIER APPLICATION NUMBER: PCT/GB96/03065
; EARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-09-077-951-68

Query Match 97.7%; Score 294; DB 4; Length 50;
Best Local Similarity 98.0%; Pred. No. 3.7e-25; Indels 1; Gaps 0;
Matches 49; Conservative 0; Mismatches 1;

QY 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50
|||
DB 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50
|||

RESULT 4

US-09-077-951-70
; Sequence 70, Application US/09077951
; Patent No. 6372888
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: PPD50093
; CURRENT APPLICATION NUMBER: US/09/077,951
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: GB 9525474.4
; EARLIER FILING DATE: 1995-12-13

; EARLIER APPLICATION NUMBER: PCT/GB96/03065
; EARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-09-077-951-70

Query Match 97.7%; Score 294; DB 4; Length 50;
Best Local Similarity 98.0%; Pred. No. 3.7e-25; Indels 1; Gaps 0;
Matches 49; Conservative 0; Mismatches 1;

QY 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50
|||
DB 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50
|||

RESULT 5

US-09-077-951-67
; Sequence 67, Application US/09077951
; Patent No. 6372888
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: PPD50093
; CURRENT APPLICATION NUMBER: US/09/077,951
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: GB 9525474.4
; EARLIER FILING DATE: 1995-12-13
; EARLIER APPLICATION NUMBER: PCT/GB96/03065
; EARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-09-077-951-67

Query Match 97.3%; Score 293; DB 4; Length 50;
Best Local Similarity 98.0%; Pred. No. 4.7e-25; Indels 1; Gaps 0;
Matches 49; Conservative 0; Mismatches 1;

QY 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50
|||
DB 1 KLCERSGTWSGVCNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYPPC 50
|||

RESULT 6

US-09-077-951-71
; Sequence 71, Application US/09077951
; Patent No. 6372888
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: PPD50093
; CURRENT APPLICATION NUMBER: US/09/077,951
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: GB 9525474.4
; EARLIER FILING DATE: 1995-12-13
; EARLIER APPLICATION NUMBER: PCT/GB96/03065
; EARLIER FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 50
; TYPE: PRT

[illegible]

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,318A
; FILING DATE: 12-JUN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9326424.0
; FILING DATE: 24-DEC-1993
; PRIOR APPLICATION DATA: PCT/GB94/02766
; APPLICATION NUMBER: PCT/GB94/02766
; FILING DATE: 19-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 224199/SER37925/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3075
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Rs-APP2
; US-08-656-318A-4

Query Match 93.4%; Score 281; DB 1; Length 51;
Best Local Similarity 92.0%; Pred. No. 9.4e-24;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCERSSGTWSGCGNNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYFPC 50
Db 2 KLCQRPSTGWSGCGNNNACKNQICIRLEKARHGSCNYVFFPAHKICICYFPC 51

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US-08-627-706-19
; Sequence 19, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 19:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-627-706-19

Query Match 93.4%; Score 281; DB 1; Length 51;
Best Local Similarity 92.0%; Pred. No. 9.4e-24;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db 2 KLCQRPSTGWSGCGNNNACKNQICIRLEKARHGSCNYVFFPAHKICICYFPC 51

RESULT 12
US-08-956-459-4
; Sequence 4, Application US/08956459
; Patent No. 5919918
; GENERAL INFORMATION:
; APPLICANT: BROEKERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,459
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/656,318
; FILING DATE: 12-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/02766
; FILING DATE: 19-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9326424.0
; FILING DATE: 24-DEC-1993
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Rs-APP2
; US-08-956-459-4

Query Match 93.4%; Score 281; DB 2; Length 51;
Best Local Similarity 92.0%; Pred. No. 9.4e-24;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCERSSGTWSGCGNNNACKNQICIRLEGAQHGSCTNYVFFPAHKICICYFPC 50
Db 2 KLCQRPSTGWSGCGNNNACKNQICIRLEKARHGSCNYVFFPAHKICICYFPC 51

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OM protein - protein search, using sw model

Run on: May 11, 2004, 16:56:34 ; Search time 42 Seconds
(without alignments)
330.437 Million cell updates/sec

Title: US-10-006-252A-10

Perfect score: 301

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pcp.*
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- 13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pcp.*
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- 18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	301	100.0	50	9	US-09-732-561-20
2	301	100.0	50	12	US-10-388-361A-36
3	301	100.0	50	13	US-10-006-252A-10
4	294	97.7	50	13	US-10-006-252A-68
5	294	97.7	50	13	US-10-006-252A-70
6	293	97.3	50	13	US-10-006-252A-67
7	292	97.0	50	13	US-10-006-252A-71
8	286	95.0	50	13	US-10-006-252A-69
9	282	93.7	51	12	US-10-388-361A-37
10	282	93.7	51	13	US-10-006-252A-11
11	281	93.4	51	9	US-09-829-381A-19
12	281	93.4	51	12	US-10-681-972-19
13	281	93.4	51	12	US-10-388-361A-35
14	281	93.4	51	13	US-10-006-252A-9
15	281	93.4	51	13	US-10-006-252A-20

16	281	93.4	51	13	US-10-006-252A-37
17	281	93.4	51	13	US-10-006-252A-77
18	281	93.4	51	15	US-10-072-809A-34
19	281	93.4	80	9	US-09-759-584-59
20	281	93.4	80	12	US-10-636-396-21
21	279	92.7	51	9	US-09-759-584-19
22	279	92.7	51	9	US-09-732-561-19
23	279	92.7	51	9	US-09-823-381A-18
24	279	92.7	51	12	US-10-681-972-18
25	279	92.7	51	12	US-10-388-361A-34
26	279	92.7	51	12	US-10-636-396-22
27	279	92.7	51	13	US-10-006-252A-8
28	279	92.7	51	15	US-10-072-809A-33
29	279	92.7	51	15	US-10-072-809A-35
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31	279	92.7	80	9	US-09-829-381A-20
32	279	92.7	80	12	US-10-681-972-20
33	277	92.0	51	13	US-10-006-252A-22
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35	277	92.0	51	13	US-10-006-252A-65
36	276	91.7	51	13	US-10-006-252A-31
37	276	91.7	51	13	US-10-006-252A-39
38	276	91.7	51	13	US-10-006-252A-44
39	276	91.7	51	13	US-10-006-252A-73
40	275	91.4	51	13	US-10-006-252A-28
41	275	91.4	51	13	US-10-006-252A-41
42	275	91.4	51	13	US-10-006-252A-42
43	275	91.4	51	13	US-10-006-252A-75
44	274	91.0	51	9	US-09-732-561-17
45	274	91.0	51	13	US-10-006-252A-23

ALIGNMENTS

RESULT 1

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; Sequence 20, Application US/09732561
; Patent No. US20020035738A1
; GENERAL INFORMATION:
;   APPLICANT: Thoma, Bart
;   APPLICANT: Terras, Franky
;   APPLICANT: Perrinckx, Iris
;   APPLICANT: Manners, John
;   APPLICANT: Kazan, Kemal
;   APPLICANT: Broekaert, Willem
;   TITLE OF INVENTION: Plant Protection Method
;   NUMBER OF SEQUENCES: 24
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: ZENECA Ag Products
;   STREET: 1800 Concord Pike
;   CITY: Wilmington
;   STATE: DE
;   COUNTRY: USA
;   ZIP: 19850
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/732,561
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/202,638
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/GB97/01672
;   FILING DATE: 20-JUN-1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Hohenschutz, Liza D.
;   REGISTRATION NUMBER: 33,712

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/ REFERENCE/DOCKET NUMBER: PPD 50165/UST
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (302) 886-1699
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 50 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ IMMEDIATE SOURCE:
/ CLONE: Rs-AFP3
US-09-732-561-20

Query Match          100.0%; Score 301; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.2e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 KLCERSSGTWSGVCNNACKNQICIRLEGAQHGSNCNVFFPAHKICICYFPC 50

RESULT 2
US-10-388-361A-36
/ Sequence 36, Application US/10388361A
/ Publication No. US20030226169A1
/ GENERAL INFORMATION:
/ APPLICANT: Van Amerongen, Aart
/ APPLICANT: Fant, Franky
/ APPLICANT: Borremans, Frans
/ APPLICANT: De Samblanx, Genoveva
/ APPLICANT: Sitj'sma, Lolke
/ APPLICANT: Melloen, Robbert
/ APPLICANT: Puijk, Wouter
/ APPLICANT: Schaaper, Wilhelmus
/ APPLICANT: Broekaert, Willem
/ APPLICANT: Van Gelder, Wilhelmus
/ APPLICANT: Rees, Sarah
/ TITLE OF INVENTION: Antifungal Proteins
/ FILE REFERENCE: 50094PPDDIV
/ CURRENT APPLICATION NUMBER: US/10/388,361A
/ CURRENT FILING DATE: 2003-03-13
/ PRIOR APPLICATION NUMBER: US 09/077,948
/ PRIOR FILING DATE: 1998-08-07
/ PRIOR APPLICATION NUMBER: PCT/GB96/03068
/ PRIOR FILING DATE: 1996-12-12
/ PRIOR APPLICATION NUMBER: GB 9606552.9
/ PRIOR FILING DATE: 1996-03-28
/ PRIOR APPLICATION NUMBER: GB 9525455.3
/ PRIOR FILING DATE: 1995-12-13
/ NUMBER OF SEQ ID NOS: 141
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 36
/ LENGTH: 50
/ TYPE: PRT
/ ORGANISM: Raphanus sativus
US-10-388-361A-36

Query Match          100.0%; Score 301; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.2e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 KLCERSSGTWSGVCNNACKNQICIRLEGAQHGSNCNVFFPAHKICICYFPC 50

RESULT 3
US-10-006-252A-10
/ Sequence 10, Application US/10006252A
/ Publication No. US20020152498A1
/ GENERAL INFORMATION:
/ APPLICANT: De Samblanx, Genoveva
/ APPLICANT: Broekaert, Willem
/ APPLICANT: Rees, Sarah
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/ APPLICANT: De Samblanx, Genoveva
/ APPLICANT: Broekaert, Willem
/ APPLICANT: Rees, Sarah
/ TITLE OF INVENTION: Antifungal Proteins
/ FILE REFERENCE: SYN-034DV
/ CURRENT APPLICATION NUMBER: US/10/006,252A
/ CURRENT FILING DATE: 2001-12-04
/ PRIOR APPLICATION NUMBER: 09/077,951
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: GB 9525474.4
/ PRIOR FILING DATE: 1995-12-13
/ PRIOR APPLICATION NUMBER: PCT/GB96/03065
/ PRIOR FILING DATE: 1996-12-12
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 10
/ LENGTH: 50
/ TYPE: PRT
/ ORGANISM: Raphanus sativus
US-10-006-252A-10

Query Match          100.0%; Score 301; DB 13; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.2e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-10-006-252A-68
/ Sequence 68, Application US/10006252A
/ Publication No. US20020152498A1
/ GENERAL INFORMATION:
/ APPLICANT: De Samblanx, Genoveva
/ APPLICANT: Broekaert, Willem
/ APPLICANT: Rees, Sarah
/ TITLE OF INVENTION: Antifungal Proteins
/ FILE REFERENCE: SYN-034DV
/ CURRENT APPLICATION NUMBER: US/10/006,252A
/ CURRENT FILING DATE: 2001-12-04
/ PRIOR APPLICATION NUMBER: 09/077,951
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: GB 9525474.4
/ PRIOR FILING DATE: 1995-12-13
/ PRIOR APPLICATION NUMBER: PCT/GB96/03065
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 68
/ LENGTH: 50
/ TYPE: PRT
/ ORGANISM: Raphanus sativus
US-10-006-252A-68

Query Match          97.7%; Score 294; DB 13; Length 50;
Best Local Similarity 98.0%; Pred. No. 5.7e-26;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 5
US-10-006-252A-70
/ Sequence 70, Application US/10006252A
/ Publication No. US20020152498A1
/ GENERAL INFORMATION:
/ APPLICANT: De Samblanx, Genoveva
/ APPLICANT: Broekaert, Willem
/ APPLICANT: Rees, Sarah
```

; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: SYN-034DV
; CURRENT APPLICATION NUMBER: US/10/006,252A
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/077,951
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: GB 9525474.4
; PRIOR FILING DATE: 1995-12-13
; PRIOR APPLICATION NUMBER: PCT/GB96/03065
; PRIOR FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-006-252A-70

Query Match 97.7%; Score 294; DB 13; Length 50;
Best Local Similarity 98.0%; Pred. No. 5.7e-26;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 KLCMRSSGTWSGVCNNACKKQCIRLEGAQHGSNCYVFFPAHKICICYFPC 50

RESULT 6
US-10-006-252A-67
; Sequence 67, Application US/10006252A
; Publication No. US20020152498A1
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: SYN-034DV
; CURRENT APPLICATION NUMBER: US/10/006,252A
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/077,951
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: GB 9525474.4
; PRIOR FILING DATE: 1995-12-13
; PRIOR APPLICATION NUMBER: PCT/GB96/03065
; PRIOR FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-006-252A-67

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Best Local Similarity 98.0%; Pred. No. 7.3e-26;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 7
US-10-006-252A-71
; Sequence 71, Application US/10006252A
; Publication No. US20020152498A1
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: SYN-034DV
; CURRENT APPLICATION NUMBER: US/10/006,252A

; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/077,951
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: GB 9525474.4
; PRIOR FILING DATE: 1995-12-13
; PRIOR APPLICATION NUMBER: PCT/GB96/03065
; PRIOR FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-006-252A-71

Query Match 97.0%; Score 292; DB 13; Length 50;
Best Local Similarity 98.0%; Pred. No. 9.5e-26;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 KLCMRSSGTWSGVCNNACKKQCIRLEGAQHGSNCYVFFPAHKICICYFPC 50

RESULT 8
US-10-006-252A-69
; Sequence 69, Application US/10006252A
; Publication No. US20020152498A1
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: SYN-034DV
; CURRENT APPLICATION NUMBER: US/10/006,252A
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/077,951
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: GB 9525474.4
; PRIOR FILING DATE: 1995-12-13
; PRIOR APPLICATION NUMBER: PCT/GB96/03065
; PRIOR FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-006-252A-69

Query Match 95.0%; Score 286; DB 13; Length 50;
Best Local Similarity 96.0%; Pred. No. 4.5e-25;
Matches 48; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 9
US-10-388-361A-37
; Sequence 37, Application US/10388361A
; Publication No. US20030226169A1
; GENERAL INFORMATION:
; APPLICANT: Van Amerongen, Aart
; APPLICANT: Fant, Franky
; APPLICANT: Borremans, Frans
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Sitjtsma, Lolke
; APPLICANT: Melloen, Robbert
; APPLICANT: Puijk, Wouter
; APPLICANT: Schaaper, Wilhelms
; APPLICANT: Broekaert, Willem

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; APPLICANT: Van Gelder, Wilhelmus
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: 50094PPDDIV
; CURRENT APPLICATION NUMBER: US/10/388.361A
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 09/077,948
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: PCT/GB96/03068
; PRIOR FILING DATE: 1996-12-12
; PRIOR APPLICATION NUMBER: GB 9606552.9
; PRIOR FILING DATE: 1996-03-28
; PRIOR APPLICATION NUMBER: GB 9525455.3
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Raphanus sativus
; ORGANISM: Raphanus sativus
US-10-388-361A-37

Query Match 93.7%; Score 282; DB 12; Length 51;
Best Local Similarity 90.0%; Pred. No. 1.3e-24;
Matches 45; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCERSGTSWGVCGNNACKNQICIRLEGAOHGSCNYVFFPAHKICICYPPC 50
Db 2 KLCERSGTSWGVCGNNACKNQICIRLEGAOHGSCNYVFFHRCICICYPC 51

RESULT 10
US-10-006-252A-11
; Sequence 11, Application US/10006252A
; Publication No. US20020152498A1
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: SYN-034DV
; CURRENT APPLICATION NUMBER: US/10/006,252A
; CURRENT FILING DATE: 2001-12-04
; PRIOR FILING DATE: 2001-07-951
; PRIOR APPLICATION NUMBER: 09/077,951
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: GB 9525474.4
; PRIOR FILING DATE: 1995-12-13
; PRIOR APPLICATION NUMBER: PCT/GB96/03065
; PRIOR FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-006-252A-11

Query Match 93.7%; Score 282; DB 13; Length 51;
Best Local Similarity 90.0%; Pred. No. 1.3e-24;
Matches 45; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCERSGTSWGVCGNNACKNQICIRLEGAOHGSCNYVFFPAHKICICYPPC 50
Db 2 KLCERSGTSWGVCGNNACKNQICIRLEGAOHGSCNYVFFHRCICICYPC 51

RESULT 11
US-09-829-381A-19
; Sequence 19, Application US/09829381A
; Patent No. US2002014306A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
```

```
; Wu, Yonnie S.
; Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, B34F
; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,381A
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-829-381A-19

Query Match 93.4%; Score 281; DB 9; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.7e-24;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCERSGTSWGVCGNNACKNQICIRLEGAOHGSCNYVFFPAHKICICYPPC 50
Db 2 KLCQRFSGTWSGVCGNNACKNQICIRLEKARHGSCNYVFFPAHKICICYPC 51

RESULT 12
US-10-681-972-19
; Sequence 19, Application US/10681972
; Publication No. US20040064850A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
; Controlling Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/10/681,972
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 51
; TYPE: PRT
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; ORGANISM: Raphanus sativus
US-10-691-972-19

Query Match      93.4%; Score 281; DB 12; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.7e-24;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLCRSSGTWSGVCNNACKNQICIRLEGAQHGSNCYVFPAAHKCIYPPC 50
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 KLCQPSGTWSGVCNNACKNQICIRLEKARHGSCNYVFPAAHKCIYPPC 51

RESULT 13
US-10-388-361A-35
; Sequence 35, Application US/10388361A
; Publication No. US20030226169A1
; GENERAL INFORMATION:
; APPLICANT: Pant, Franky
; APPLICANT: Borremans, Frans
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Sitjtama, Lolke
; APPLICANT: Melloen, Robbert
; APPLICANT: Puijk, Wouter
; APPLICANT: Schaaper, Wilhelmus
; APPLICANT: Broekaert, Willem
; APPLICANT: Van Gelder, Wilhelmus
; APPLICANT: Rees, Sarah
; FILE OF INVENTION: Antifungal Proteins
; CURRENT APPLICATION NUMBER: US/10/388,361A
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 09/077,948
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: PCT/GB96/03068
; PRIOR FILING DATE: 1996-12-12
; PRIOR APPLICATION NUMBER: GB 9606552.9
; PRIOR FILING DATE: 1996-03-28
; PRIOR APPLICATION NUMBER: GB 9525455.3
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-388-361A-35

Query Match      93.4%; Score 281; DB 12; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.7e-24;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLCRSSGTWSGVCNNACKNQICIRLEGAQHGSNCYVFPAAHKCIYPPC 50
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 KLCQPSGTWSGVCNNACKNQICIRLEKARHGSCNYVFPAAHKCIYPPC 51

RESULT 14
US-10-006-252A-9
; Sequence 9, Application US/10006252A
; Publication No. US20020152498A1
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; FILE OF INVENTION: Antifungal Proteins
; CURRENT APPLICATION NUMBER: US/10/006,252A
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/077,951
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: GB 9525474.4
; PRIOR FILING DATE: 1995-12-13
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; PRIOR APPLICATION NUMBER: PCT/GB96/03065
; PRIOR FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-006-252A-9

Query Match      93.4%; Score 281; DB 13; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.7e-24;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLCRSSGTWSGVCNNACKNQICIRLEGAQHGSNCYVFPAAHKCIYPPC 50
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Db 2 KLCQPSGTWSGVCNNACKNQICIRLEKARHGSCNYVFPAAHKCIYPPC 51

RESULT 15
US-10-006-252A-20
; Sequence 20, Application US/10006252A
; Publication No. US20020152498A1
; GENERAL INFORMATION:
; APPLICANT: De Samblanx, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: SYN-034DV
; CURRENT APPLICATION NUMBER: US/10/006,252A
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/077,951
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: GB 9525474.4
; PRIOR FILING DATE: 1995-12-13
; PRIOR APPLICATION NUMBER: PCT/GB96/03065
; PRIOR FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Raphanus sativus
US-10-006-252A-20

Query Match      93.4%; Score 281; DB 13; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.7e-24;
Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db 2 KLCQPSGTWSGVCNNACKNQICIRLEKARHGSCNYVFPAAHKCIYPPC 51

Search completed: May 11, 2004, 17:00:01
Job time : 56 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2004, 16:54:24 ; Search time 20 Seconds
(without alignments)
240.479 Million cell updates/sec

Title: US-10-006-252A-10
Perfect score: 301
Sequence: 1 KLCERSSGTWSGCGNNAC.....QHGSNCYVFPAAKICVYPC 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	301	100.0	79	2 T10243	antifungal protein
2	301	100.0	79	2 T07917	antifungal protein
3	282	93.7	80	2 T10183	antifungal protein
4	281	93.4	80	2 T10623	antifungal protein
5	279	92.7	80	2 T10176	antifungal protein
6	279	92.7	80	2 T02622	probable antifunga
7	274	91.0	80	2 F96787	protein t4O12.7 [i
8	272	90.4	80	2 T02621	probable antifunga
9	167	55.5	56	2 G86328	hypothetical prote
10	162	53.8	50	2 S68221	defensin AMP1 - Da
11	151	50.2	30	2 S28991	antifungal protein
12	145	48.2	161	2 S12246	anther-specific pr
13	142	47.2	27	2 S28989	antifungal protein
14	140.5	46.7	49	2 S66219	defensin AMP1 - C1
15	138	45.8	25	2 S28993	antifungal protein
16	137	45.5	27	2 S28995	antifungal protein
17	136	45.2	26	2 S28994	antifungal protein
18	134.5	44.7	54	2 S66220	defensin APp1 - He
19	134	44.5	27	2 S28990	antifungal protein
20	129.5	43.0	50	2 S66218	defensin AMP1 - Ae
21	116.5	38.7	80	2 F96591	probable gamma-thi
22	116.5	38.7	83	2 T14866	probable gamma-thi
23	105.5	35.0	152	2 S46272	anther-specific pr
24	101.5	33.7	93	2 T03673	piti protein (Clon
25	82.5	27.4	105	2 S57809	gamma-thionin-like
26	80.5	26.7	55	2 D96636	unknown protein, 8
27	77.5	25.7	47	2 A58319	gamma-zeathionin
28	75.5	25.1	47	2 S11529	gamma-purothionin
29	75.5	25.1	105	2 S23574	thionin precursor,

30	74.5	24.8	47	2 S69146	gamma-thionin SI-a
31	74.5	24.8	47	2 S13849	hordothionin gamma
32	74.5	24.8	47	2 S69144	gamma-thionin SI-a
33	74	24.6	1408	2 S16148	gene serrate prote
34	73.5	24.4	2233	2 T28669	surface protein 51
35	73	24.3	64	1 NTSR3B	neurotoxin III - s
36	73	24.3	85	1 NTSR2A	neurotoxin II prec
37	72.5	24.1	73	2 D84433	proteinase inhibit
38	72	23.9	20	2 S66222	defensin AMP2 - Da
39	71.5	23.8	81	2 T02667	proteinase inhibit
40	70.5	23.4	72	2 T06599	disease resistance
41	70.5	23.4	82	2 JC7897	defensin 1 precurs
42	70.5	23.4	1394	2 A35626	transforming growt
43	70	23.3	74	2 T06766	disease resistance
44	69.5	23.1	47	2 S11530	purothionin gamma
45	69	22.9	65	1 NTSREB	neurotoxin XI - sc

ALIGNMENTS

RESULT 1

T10243
antifungal protein 3 precursor - radish
C/Species: Raphanus sativus (radish)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C/Accession: T10243
R/Terras, F.R.G.; Goderis, I.J.; Penninckx, I.J.; Osborn, R.W.; Broekaert, W.F.
submitted to the EMBL Data Library, April 1996
A/Reference number: Z16994
A/Accession: T10243
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-79 <TER>
A/Cross-references: EMBL:X97319
A/Experimental source: cultivar Ronde Rode Kleine Witpunt
C/Genetics:
A/Gene: APP3
C/Superfamily: gamma-thionin
C/Keywords: antifungal
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-79/Product: antifungal protein 3 #status predicted <MAT>

Query Match 100.0%; Score 301; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLCERSSGTWSGCGNNACNQCIRLEGAHQHSCNYVFPAAKICVYPC 50
Db 30 KLCERSSGTWSGCGNNACNQCIRLEGAHQHSCNYVFPAAKICVYPC 79

RESULT 2

T07917
antifungal protein - rape
C/Species: Brassica napus (rape)
C/Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jun-2000
C/Accession: T07917
R/Sohn, U.; Lee, C.M.; Lee, M.H.; Kim, J.H.
submitted to the EMBL Data Library, May 1996
A/Reference number: Z16214
A/Accession: T07917
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-79 <SOH>
A/Cross-references: EMBL:U59459; NID:gl399229; PIDN:AAB03224.1; PID:gl399230
A/Experimental source: cv. Naehan
C/Superfamily: gamma-thionin

Query Match 100.0%; Score 301; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A;Accession: D84655
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-80 <STO>
 A;Cross-references: GB:AE002093; NID:g3413711; PIDN:AAC31234.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g26010; T19L18.18
 A;Map position: 2
 A;Introns: 22/1
 C;Superfamily: gamma-thionin

Query Match 92.7%; Score 279; DB 2; Length 80;
 Best Local Similarity 90.0%; Pred. No. 5.2e-23;
 Matches 45; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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 Db 31 KLCERPSGTWGVCGNSACKKQCNINLEGAKHGSNCYVFFPAHKICICYFPC 80

RESULT 7

P96787
 C;Species: Arabidopsis thaliana (mouse-ear cross)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
 C;Accession: P96787
 R;Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chinn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: P96787
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-80 <STO>
 A;Cross-references: GB:AE005173; NID:g6721100; PIDN:AAF26754.1; GSPDB:GN00141
 C;Genetics:
 A;Gene: T4012.7
 A;Map position: 1
 C;Superfamily: gamma-thionin

Query Match 91.0%; Score 274; DB 2; Length 80;
 Best Local Similarity 90.0%; Pred. No. 1.8e-22;
 Matches 45; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLCERSGTWGVCGNNAKQKQIRLEGAQHGSNCYVFFPAHKICICYFPC 50
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 31 KLCERPSGTWGVCGNSACKKQCNINLEKARHGSNCYVFFPAHKICICYFPC 80

RESULT 8

T02621
 Probable antifungal protein T19L18.17 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cross)
 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
 C;Accession: T02621; E84655
 R;Roundley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
 submitted to the EMBL Data Library, August 1998
 A;Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.
 A;Reference number: Z14681
 A;Accession: T02621
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-80 <ROU>
 A;Cross-references: EMBL:AC004747; NID:g3413696; PID:g3413721
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon,
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: E84655
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-80 <STO>
 A;Cross-references: GB:AE002093; NID:g3413721; PIDN:AAC31244.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g26020; T19L18.17
 A;Map position: 2
 A;Introns: 22/1
 C;Superfamily: gamma-thionin

Query Match 90.4%; Score 272; DB 2; Length 80;
 Best Local Similarity 88.0%; Pred. No. 2.9e-22;
 Matches 44; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLCERSGTWGVCGNNAKQKQIRLEGAQHGSNCYVFFPAHKICICYFPC 50
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 31 KLCERPSGTWGVCGNSACKKQCNINLEGAKHGSNCYVFFPAHKICICYFPC 80

RESULT 9

G86328
 Hypothetical protein F14P1.6 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cross)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
 C;Accession: G86328
 R;Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon,
 Chinn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: G86328
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-56 <STO>
 A;Cross-references: GB:AE005172; NID:g9795584; PIDN:AAF98402.1; GSPDB:GN00141
 C;Genetics:
 A;Map position: 1

Query Match 55.5%; Score 167; DB 2; Length 56;
 Best Local Similarity 52.0%; Pred. No. 3.2e-11;
 Matches 26; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

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 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 7 RICERSKTWTGFCNTRGCDSCQCKRWERASHGACHAQPFGFACFCYFNC 56

RESULT 10

S66221
 defensin AMP1 - Dahlia merckii
 N;Alternate names: seed antifungal protein
 C;Species: Dahlia merckii
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
 C;Accession: S66221
 R;Osborn, R.W.; de Samblanx, G.W.; Thevissen, K.; Goderis, I.; Torrekens, S.; van Lee,
 FEBS Lett. 368, 257-262, 1995
 A;Title: Isolation and characterisation of plant defensins from seeds of Asteraceae,
 A;Reference number: S66218; MUID:95354848; PMID:7628617
 A;Accession: S66221
 A;Molecule type: protein
 A;Residues: 1-50 <OSB>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 16:50:53 ; Search time 11 Seconds
(without alignments)
236.683 Million cell updates/sec

Title: US-10-006-252A-10

Perfect score: 301

Sequence: 1 KLCERSGTSWGVCGNNAC.....QHGSQNVFPAHKICICYPC 50

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	301	100.0	79	1	APP3_BRANA
2	301	100.0	79	1	APP3_RAPSA
3	282	93.7	80	1	APP4_RAPSA
4	281	93.4	80	1	APP2_RAPSA
5	279	92.7	51	1	APP1_SINAL
6	279	92.7	80	1	APP1_BRANA
7	279	92.7	80	1	APP2_ARATH
8	274	91.0	80	1	APP1_ARATH
9	273	90.7	51	1	APP2_SINAL
10	272	90.4	80	1	APP3_ARATH
11	272	90.4	80	1	APP4_ARATH
12	211.5	70.3	52	1	APP2_SINAL
13	145	48.2	161	1	ASPI_HELAN
14	142	47.2	27	1	APP1_BRARA
15	134	44.5	27	1	APP2_BRARA
16	124	41.2	23	1	APP2_BRANA
17	90.5	30.1	75	1	DEFL_CAPAN
18	85.5	28.4	106	1	THGL_NICPA
19	83.5	27.7	52	1	DEP2_SPIOL
20	77.5	25.7	47	1	THG1_MAIZE
21	75.5	25.1	47	1	THG1_WHEAT
22	75.5	25.1	105	1	THGF_TOBAC
23	74.5	24.8	47	1	SA21_SORBI
24	74.5	24.8	47	1	SIA3_SORBI
25	74.5	24.8	47	1	THG_HORVU
26	74	24.6	46	1	PSDI_PEA
27	74	24.6	1408	1	SERE_DROME
28	73	24.3	64	1	SCX2_LEIQH
29	73	24.3	64	1	SCX3_BUTOO
30	73	24.3	85	1	SCX2_ANDAU
31	73	24.3	85	1	SCXA_ANDAU
32	72.5	24.1	73	1	THG4_ARATH
33	71	23.6	46	1	AX2_ETVU

34	70.5	23.4	47	1	PSD2_PEA
35	70.5	23.4	72	1	D230_PEA
36	70.5	23.4	1394	1	LTBS_HUMAN
37	70.5	23.4	1595	1	LTBL_HUMAN
38	70	23.3	74	1	DR39_PEA
39	69.5	23.1	47	1	THG2_WHEAT
40	69	22.9	65	1	SCXB_BUTOO
41	68	22.6	65	1	ITHC_HIRME
42	68	22.6	670	1	S213_RAT
43	67	22.3	64	1	SCX5_LEIQH
44	67	22.3	1213	1	JAG3_BRARE
45	66.5	22.1	47	1	THGC_VIGUN

ALIGNMENTS

RESULT 1
APP3_BRANA STANDARD; PRT; 79 AA.
AC Q393I3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 3 precursor (APP3).
GN APP3.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Naehan.
RA Sohn U., Lee C.M., Lee M.H., Kim J.H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the plant defensin family.

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CC -----
CC EMBL; U59459; AAB03224.1; -
CC PIR; T07917; T07917.
CC HSSP; P30231; 1AYJ.

DR InterPro; IPR008176; Gamma-thionin.
DR InterPro; IPR003614; Knot1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Furothionin; 1.
DR SMART; SM00505; Knot1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.

FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 79 CYSTEINE-RICH ANTIFUNGAL PROTEIN 3.
FT DISULFID 43 64 BY SIMILARITY.
FT DISULFID 49 73 BY SIMILARITY.
FT DISULFID 53 75 BY SIMILARITY.

SQ SEQUENCE 79 AA; 8555 MW; 3B5289FCFEA48936 CRC64;

Query Match 100.0%; Score 301; DB 1; Length 79;

Best Local Similarity 100.0%; Pred. No. 5.4e-27; Indels 0; Gaps 0;

Matches 50; Conservative 0; Mismatches 0;

QY 1 KLCERSGTSWGVCGNNACNQICIRLEGAGHSCNYYVPAHKICICYPC 50

|||||

Db 30 KLCERSGTWSGCGNNACKNQCTIRLEGAQHGSNCYVFFPAHKICICYFPC 79

RESULT 2

APP3_RAPSA STANDARD; PRT; 79 AA.
AC O24332;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 3 precursor (APP3).
GN APP3.
OS Raphanus sativus (Radish).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Raphanus.
OX NCBI_TaxID=3726;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Ronde Kleine Witpunt; TISSUE=Seed;
RA Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
RA Broekaert W.F.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the plant defensin family.

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DR EMBL; X97319; CAA65984.1; -.
DR PIR; T10243; T10243.
DR HSP; P30231; IAYJ.
DR InterPro; IPR008176; Gamma-thionin.
DR InterPro; IPR003614; Knott1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.
DR SMART; SM00505; Knott1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
KW Plant defense; Fungicide; Signal; Multigene family.
KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 79 Cysteine-rich antifungal protein 3.
FT MOD_RES 30 79 BY SIMILARITY.
FT DISULFID 32 79 BY SIMILARITY.
FT DISULFID 43 64 BY SIMILARITY.
FT DISULFID 49 73 BY SIMILARITY.
FT DISULFID 53 75 BY SIMILARITY.
SQ SEQUENCE 79 AA; 8479 MW; BAF80465DB48548 CRC64;

Query Match 100.0%; Score 301; DB 1; Length 79;
Best Local Similarity 100.0%; Pred. No. 5.4e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLCERSGTWSGCGNNACKNQCTIRLEGAQHGSNCYVFFPAHKICICYFPC 50
Db 30 KLCERSGTWSGCGNNACKNQCTIRLEGAQHGSNCYVFFPAHKICICYFPC 79

RESULT 3

APP4_RAPSA STANDARD; PRT; 80 AA.
AC O24331;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 4 precursor (APP4).
GN APP4.
OS Raphanus sativus (Radish).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Raphanus.
OX NCBI_TaxID=3726;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Ronde Kleine Witpunt; TISSUE=Seed;
RA Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
RA Broekaert W.F.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the plant defensin family.

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DR EMBL; X97318; CAA65983.1; -.
DR PIR; T10183; T10183.
DR HSP; P30231; IAYJ.
DR InterPro; IPR008176; Gamma-thionin.
DR InterPro; IPR003614; Knott1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.
DR SMART; SM00505; Knott1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
KW Plant defense; Fungicide; Signal; Multigene family.
KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 80 Cysteine-rich antifungal protein 4.
FT MOD_RES 30 80 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT DISULFID 33 80 BY SIMILARITY.
FT DISULFID 44 65 BY SIMILARITY.
FT DISULFID 50 74 BY SIMILARITY.
FT DISULFID 54 76 BY SIMILARITY.
SQ SEQUENCE 80 AA; 8873 MW; B5F667B6441818C9 CRC64;

Query Match 93.7%; Score 282; DB 1; Length 80;
Best Local Similarity 90.0%; Pred. No. 6.9e-25;
Matches 45; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLCERSGTWSGCGNNACKNQCTIRLEGAQHGSNCYVFFPAHKICICYFPC 50
Db 31 KLCERSGTWSGCGNNACKNQCTIRLEGAQHGSNCYVFFPAHKICICYFPC 80

RESULT 4

APP2_RAPSA STANDARD; PRT; 80 AA.
AC P30230;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 2 precursor (APP2).
GN APP2.
OS Raphanus sativus (Radish).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Raphanus.
OX NCBI_TaxID=3726;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Ronde Kleine Witpunt; TISSUE=Seed;
RA Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
RA Broekaert W.F.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the plant defensin family.

RA Cammue B.P.A., Broekaert W.F.;
 RT "Small cysteine-rich antifungal proteins from radish: their role in
 RL host defense.";
 RN Plant Cell 7:573-588(1995).
 RP [2]
 RC SEQUENCE OF 30-65.
 RX TISSUE=Seed;
 RA MEDLINE=92348373; PubMed=1639777;
 RA Terras F.R.G., Schoofs H.W.E., de Bolle M.F.C., van Leuven F.,
 RA Rees S.B., Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "Analysis of two novel classes of plant antifungal proteins from
 RT radish (Raphanus sativus L.) seeds.";
 RL J. Biol. Chem. 267:15301-15309(1992).
 CC -1- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the plant defensin family.
 CC -----
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 CC -----
 DR EMBL: U18556; AAA69540.1; -;
 DR PIR: T10823; T10823.
 DR HSP: P30231; IAYJ.
 DR InterPro: IPR008176; Gamma-thionin.
 DR InterPro: IPR003614; Knott1.
 DR Pfam: PF00304; Gamma-thionin; 1.
 DR ProDom: PD002594; G_Purothionin; 1.
 DR SMART: SM00505; Knott1; 1.
 DR PROSITE: PS00940; GAMMA-THIONIN; 1.
 DR Plant defense; Fungicide; Signal; Multigene family;
 KW Pyrrolidone carboxylic acid.
 KW Pyrolidone carboxylic acid.
 FT SIGNAL 1 29
 FT CHAIN 30 30 CYSTEINE-RICH ANTIFUNGAL PROTEIN 2.
 FT MOD RES 30 30 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 33 80 BY SIMILARITY.
 FT DISULFID 44 65 BY SIMILARITY.
 FT DISULFID 50 74 BY SIMILARITY.
 FT DISULFID 54 76 BY SIMILARITY.
 SQ SEQUENCE 80 AA; 8875 MW; 746110D9A8CE6370 CRC64;
 Query Match 93.48; Score 281; DB 1; Length 80;
 Best Local Similarity 92.0%; Pred. No. 8.9e-25;
 Matches 46; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 KLCRRSGTWSGVCNNACKNQICRLGAGHGSNNYVPPAHKICICYFPC 50
 Db 31 KLCRRPSGTWSGVCNNACKNQICRLGAGHGSNNYVPPAHKICICYFPC 80
 RESULT 5
 APPI_SINAL
 ID _APPI_SINAL STANDARD; PRT; 51 AA.
 AC P30231;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 1 (APPI) (M1).
 OS Sinapis alba (White mustard) (Brassica hirta).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Sinapis.
 OX NCBI_TaxID=3728;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=96433791; PubMed=8836771;
 RA Neumann G.M., Condron R., Polya G.M.;

RT "Purification and mass spectrometry-based sequencing of yellow
 RT mustard (Sinapis alba L.) 6 kDa proteins. Identification as
 RL antifungal proteins.";
 RN Int. J. Pept. Protein Res. 47:437-446(1996).
 RP [2]
 RC SEQUENCE OF 1-25.
 RX TISSUE=Seed;
 RA MEDLINE=93138130; PubMed=8422949;
 RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RT Brassicaceae species.";
 RL FEBS Lett. 316:233-240(1993).
 CC [3]
 CC STRUCTURE BY NMR.
 CC MEDLINE=96300344; PubMed=9636715;
 CC Fant P., Vranken W.F., Broekaert W.F., Borremans F.A.M.;
 CC "Determination of the three-dimensional solution structure of Raphanus
 CC sativus antifungal protein 1 by 1H NMR.";
 CC J. Mol. Biol. 279:257-270(1998).
 CC -1- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -1- SUBUNIT: Forms oligomers in its native state.
 CC -1- MASS SPECTROMETRY: MW=5677; MW ERR=1.0; METHOD=Electrospray.
 CC -1- SIMILARITY: Belongs to the plant defensin family.
 CC -----
 DR PDB: IAYJ; 28-JAN-98.
 DR InterPro: IPR008176; Gamma-thionin.
 DR InterPro: IPR003614; Knott1.
 DR Pfam: PF00304; Gamma-thionin; 1.
 DR ProDom: PD002594; G_Purothionin; 1.
 DR SMART: SM00505; Knott1; 1.
 DR PROSITE: PS00940; GAMMA-THIONIN; 1.
 DR Plant defense; Fungicide; 3D-structure; Pyrrolidone carboxylic acid.
 KW MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 KW DISULFID 4 51
 KW DISULFID 15 36
 KW DISULFID 21 45
 KW DISULFID 25 47
 KW STRAND 4 7
 KW STRAND 18 28
 KW STRAND 34 37
 KW STRAND 44 49
 SQ SEQUENCE 51 AA; 5695 MW; 770990E72DD1C469 CRC64;
 Query Match 92.7%; Score 279; DB 1; Length 51;
 Best Local Similarity 92.0%; Pred. No. 9.8e-25;
 Matches 46; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 KLCRRSGTWSGVCNNACKNQICRLGAGHGSNNYVPPAHKICICYFPC 50
 Db 2 KLCRRPSGTWSGVCNNACKNQICRLGAGHGSNNYVPPAHKICICYFPC 51
 RESULT 6
 APPI_BRANA
 ID _APPI_BRANA STANDARD; PRT; 80 AA.
 AC P30225; Q41163;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 1 precursor (APPI).
 GN APPI.
 OS Brassica napus (Rape), and
 OS Raphanus sativus (Radish).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708; 3726;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=R.sativus; STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
 RX MEDLINE=95299350; PubMed=7780308;
 RA Terras F.R.G., Eggermont K., Kovaleva V., Raikhel N.V., Osborn R.W.,

```

DE   Probable cysteine-rich antifungal protein At2g26010 precursor (APP).
GN   AT2g26010 OR T19J18.18.
DN   Arabidopsis thaliana (Mouse-ear cress).
OS   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC   NCBI_taxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAINE=cv. Columbia;
RX   MEDLINE=20083487; PubMed=10517197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Renning C.M., Koo H.L.,
RA   Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA   Tallon L.J., Gill J.E., Adams W.C., Carrera A.J., Creasy T.H.,
RA   Goodman H.M., Somerville C.R., Cohenhaver G.P., Preuss D.,
RA   Nirman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA   Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana";
RL   Nature 402:761-768(1999).
CC   -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC   cations (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: Belongs to the plant defensin family.
CC   -----
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EMBL AC004747; AAC13234.1; -.
PIR T02622; T02622.
HSSP P30231; IAYJ.
DR DR InterPro; IPR008176; Gamma-thionin.
DR DR InterPro; IPR003614; Knot1.
DR DR Pfam; PF00304; Gamma-thionin; 1.
DR DR ProDom; PD002594; G_Purochionin; 1.
DR DR SMART; SM00505; Knot1; 1.
DR DR PROSITE; PS00940; GAMMA_THIONIN; 1.
KW Plant defense; Fungicide; Signal; Multigene family;
FT Pyrolydione carboxylic acid.
FT SIGNAL 1 29
FT CHAIN 30 80
FT FT PROBABLE CYSTEINE-RICH ANTIFUNGAL PROTEIN
FT FT AR2G26010.
FT FT PYROLYDIONE CARBOXYLIC ACID (BY
FT FT SIMILARITY).
FT FT DISULFID 33 80
FT FT BY SIMILARITY.
FT FT DISULFID 44 65
FT FT BY SIMILARITY.
FT FT DISULFID 50 74
FT FT BY SIMILARITY.
FT FT DISULFID 54 76
FT FT BY SIMILARITY.
FT FT SEQUENCE 80 AA; 8580 MW; 99E1E0D443AD67B CRC64;
SQ
Query Match 92.7%; Score 279; DB 1; Length 80;
Best Local Similarity 90.0%; Pred.No.1.5e-24;
Matches 45; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 KLCSRSSTWSGVCGNNACKNQCIRLEGAHGSCNVVFPAAKICICYPPC 50
DB 31 KLCKPSGTWSGVCGNSACKNCQINLEGAKGSCNVVFPAAKICICYPC 80
RESULT 8
APPL APATH STANDARD; PRT; 80 AA.
ID AC P30224; Q42179;
DT 01-APR-1993 (Rel. 25, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE Cysteine-rich antifungal protein 1 precursor (AFp1) (Anther-specific
 DN protein S18 homolog).
 GN AFp1 OR PFp1.1 OR AtFG5830 OR T4012.6 OR T4012.7.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 CX NCBI_taxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Raynal M.; Greillet F.; Laudie M.; Meyer Y.; Cooke R.; Delseny M.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=Seed;
 RA Raynal M.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99178804; PubMed=10080719;
 RA Williams R.W.; Clark S.E.; Meyerowitz E.M.;
 RL "Genetic and physical characterization of a region of Arabidopsis
 chromosome 1 containing the CLAVATA1 gene.";
 RL Plant Mol. Biol. 39:171-176(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A.; Ecker J.R.; Palm C.J.; Federspiel N.A.; Kaul S.;
 RA White O.; Alonso J.; Altati H.; Araujo R.; Bowman C.L.; Brooks S.Y.;
 RA Buehler E.; Chan A.; Chao Q.; Chen H.; Cheuk R.F.; Chin C.W.;
 RA Chung M.K.; Conn L.; Conway A.B.; Conway A.R.; Creasy T.H.; Dewar K.;
 RA Dunn P.; Egtu P.; Feldblyum T.V.; Feng J.-D.; Fong B.; Fujii C.Y.;
 RA Gill J.E.; Goldsmith A.D.; Haas B.; Hansen N.F.; Hughes B.; Huizar L.;
 RA Hunter J.L.; Jenkins J.; Johnson-Hopson C.; Khan S.; Khaykin E.;
 RA Kim C.J.; Koo H.S.; Kremenetskaia I.; Kurtz D.B.; Kwan A.; Lam B.;
 RA Langin-Hooper S.; Lee A.; Lee J.M.; Lenz C.A.; Li J.H.; Li Y.-P.;
 RA Lin X.; Liu S.X.; Liu Z.A.; Luros J.S.; Maiti R.; Marziani A.;
 RA Militscher J.; Miranda M.; Nguyen M.; Nierman W.C.; Osborne B.I.;
 RA Pai G.; Peterson J.; Pham P.K.; Rizzo M.; Rooney T.; Rowley D.;
 RA Sakano H.; Salzberg S.L.; Schwartz J.R.; Shinn P.; Southwick A.M.;
 RA Sun H.; Tallon L.J.; Tambunga G.; Toriumi M.J.; Town C.D.;
 RA Uterback T.; Van Aken S.; Vaysberg M.; Vysotskaia V.S.; Walker M.;
 RA Wu D.; Yu G.; Fraser C.M.; Venter J.C.; Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana";
 RL Nature 408:816-820(2000).
 RN [5]
 RP SEQUENCE OF 30-56.
 RC TISSUE=Seed;
 RX MEDLINE=93138130; PubMed=8422949;
 RA Terras F.R.G.; Torrekens S.; van Leuven F.; Osborn R.W.;
 RA Vanderleyden J.; Cammue B.P.A.; Broekaert W.F.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 Brassicaceae species.";
 RL FEBS Lett. 316:233-240(1993).
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -!- SUBUNIT: Forms oligomers in its native state.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z27258; CAA81770.1; -
 CC EMBL; Z29957; CAA82845.1; -

DR EMBL; X91916; CAA63009.1; -
 DR EMBL; AF049870; AAD02502.1; -
 DR EMBL; AC007396; AAF26754.1; -
 DR PIR; F96787; F96787.
 DR HSSP; P30231; IAYJ.
 DR InterPro; IPR008176; Gamma-thionin.
 DR InterPro; IPR003614; Knot1.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G_Purothionin; 1.
 DR SMART; SM00305; Knot1; 1.
 DR PROSITE; PS00940; GAMMA_THIONIN; 1.
 DR Plant defense; Fungicide; Signal; Multigene family;
 KW Pyroliidone carboxylic acid.
 FT SIGNAL 1 29
 FT CHAIN 30 80 CYSTEINE-RICH ANTIFUNGAL PROTEIN 1.
 FT MOD RES 30 30 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 33 80 BY SIMILARITY.
 FT DISULFID 44 65 BY SIMILARITY.
 FT DISULFID 50 74 BY SIMILARITY.
 FT DISULFID 54 76 BY SIMILARITY.
 FT CONFLICT 33 33 C -> F (IN REF. 1).
 SQ SEQUENCE 80 AA; 8709 MW; 99F34A8DA360441F CRC64;
 Query Match 91.0%; Score 274; DB 1; Length 80;
 Best Local Similarity 90.0%; Pred. NO. 5.3e-24;
 Matches 45; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 KLCERSSTGWSGVCNNACKNQICIRLEGAQHGSNCYVFPAAKCICTFPC 50
 Db 31 KLCERSSTGWSGVCNNACKNQICINLEKARHGSNCYVFPAAKCICTFPC 80
 RESULT 9
 ID AF2A SIGNAL STANDARD; PRT; 51 AA.
 AC P30232;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 2A (AFP2A) (M2A).
 OS Sinapis alba (White mustard) (Brassica hirta).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Sinapis.
 CX NCBI_TaxID=3728;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=96433791; PubMed=8836771;
 RA Neumann G.M.; Condron R.; Polya G.M.;
 RT "Purification and mass spectrometry-based sequencing of yellow
 RT mustard (Sinapis alba L.) 6 kDa proteins. Identification as
 RT antifungal proteins.";
 RL Int. J. Pept. Protein Res. 47:437-446(1996).
 RN [2]
 RP SEQUENCE OF 1-26.
 RC TISSUE=Seed;
 RX MEDLINE=93138130; PubMed=8422949;
 RA Terras F.R.G.; Torrekens S.; van Leuven F.; Osborn R.W.;
 RA Vanderleyden J.; Cammue B.P.A.; Broekaert W.F.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RT Brassicaceae species.";
 RL FEBS Lett. 316:233-240(1993).
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -!- SUBUNIT: Forms oligomers in its native state.
 CC -!- MASS SPECTROMETRY: MW=5705; MW_ERR=0.8; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 CC HSSP; P30231; IAYJ.
 DR InterPro; IPR008176; Gamma-thionin.
 DR InterPro; IPR003614; Knot1.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G_Purothionin; 1.

DR	SMART; SMO0505; Knot1; 1.
DR	PRO317; PS00940; GAMMA THIONIN; 1.
KW	Fungicide; Phosphorylation; Pyrrolidone carboxylic acid.
FT	FT MOD_RES 1 1
FT	FT MOD_RES 8 8
FT	FT DISULFID 4 51
FT	FT DISULFID 15 36
FT	FT DISULFID 21 45
FT	FT DISULFID 25 47
SQ	SEQUENCE 51 AA; 5722 MW; 1C7F50E72DC945B1 C8C64;

Query Match 90.7%; Score 273; DB 1; Length 51;
Best Local Similarity 88.0%; Pred. No. 4.5e-24;
Matches 44; Conservative 3; Mismatches 3; Indels 0;

Qy

1 KLCRSSGTWSGCGNNACKNQICIRLEGAQHGSCTVYFPAHKCIYFPC 50
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

Dd

2 KLORPSGTWSGCGNNACKNQICINLEKARHGSCTVYFPAHKCIYFPC 51
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

RESULT 10

000001	10	REF3	ARATH	STANDARD;	PRT;	80	AA.
1C	AD	AF3	ARATH				
1D	AC	O80954;					
1E	DT	16-CCT-2001	(Rel. 40, Created)				
1F	DT	16-CCT-2001	(Rel. 40, Last sequence update)				
1G	DT	28-FEB-2003	(Rel. 41, Last annotation update)				
1H	DE	Probable	cysteine-rich antifungal protein A2G26020 precursor (APP).				
1I	DE	AT2G26020	OR T1918.17				
1J	GN	Arabidopsis	thaliana (Mouse-ear cross).				
1K	OS	Eukaryota;	Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
1L	OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;					
1M	OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.					
1N	OX	NCBI	TaxID=3702;				
1O	CC	[1]					
1P	CC	SEQUENCE	FROM N.A.				
1Q	RP	STRAIN=cv.	Columbia;				
1R	CC	MEDLINE=20083487;	PubMed=10617197;				
1S	RY	Lin X.,	Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,				
1T	RA	Fujii C.X.,	Mason T.M., Bowman K.A., Barnstead M.E., Feldblyum T.V.,				
1U	RA	Buell C.K.,	Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,				
1V	RA	Moffat K.S.,	Cronin L.A., Lee J.C., Van Aken S., Unayam L.,				
1W	RA	Tallon L.J.,	Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,				
1X	RA	Goodman H.M.,	Somerville C.R., Copenhaver G.P., Preuss D.,				
1Y	RA	Nierman W.C.,	White O., Eisen J.A., Salzberg S.L., Fraser C.M.,				
1Z	RA	Venter J.C.;					
20	CC	"Sequence	and analysis of chromosome 2 of the plant Arabidopsis				
21	RT	thaliana";					
22	RL	Nature	402:761-768 (1999).				
23	CC	!- FUNCTION:	Possesses antifungal activity sensitive to inorganic				
24	CC	cations (By	similarity).				
25	CC	!- SUBCELLULAR	LOCATION: Secreted (By similarity).				
26	CC	!- SIMILARITY:	belongs to the plant defensin family.				

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CC	EMBL; AC004747; AAC31244.1; -.
DR	PIR; T02621; T02621.
DR	HSSP; P30231; IAYG.
DR	Interpro; IPR008176; Gamma-thionin.
DR	Interpro; IPR003614; Knot1.
DR	Pfam; PF00304; Gamma-thionin; 1.
DR	ProDom; PD002594; G_Purothionin; 1.
DR	SMART; SM00505; Knot1; 1.
DR	PROSITE; PS00940; GAMMA_THIONIN; 1.
DR	Plant defense; Fungicide; Signal; Multigene family;
KW	Pyroolidene carboxylic acid.

FT	SIGNAL	1	29	BY SIMILARITY.
FT	CHAIN	30	80	PROBABLE CYSTEINE-RICH ANTIFUNGAL PROTEIN.
FT				AT236020.
FT	MOD_RES	30	30	PYROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
FT				BY SIMILARITY.
FT	DISULFID	33	80	BY SIMILARITY.
FT	DISULFID	44	65	BY SIMILARITY.
FT	DISULFID	50	74	BY SIMILARITY.
FT	DISULFID	54	76	BY SIMILARITY.
SQ	SEQUENCE	80 AA:	8640 MW:	81B106059BAFFCC7 CRC64;

Query Match 90.4%; Score 272; DB 1; Length 80;
Best Local Similarity 88.0%; Pred. No. 8.8e-24;
Matches 44; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLCERSSTGSGVCGNNAACNQICIRLEGAOHGSCNVVFPAHKCICVFP 50
|||:|||||:|||||:|||||:|||||:|||||:
Dd 31 KLCEKPSGTSGVCGNSNACNQICINLEGAKHGSCNVVFPAHKCICVPC 80

RESULT 11

```

RESULT 11
APP4 ARATH
ID APP4 ARATH STANDARD; PRT; 80 AA.
DT DT Q9FI23; P82786;
DT DT 16-OCT-2001 (Rel. 40, Created)
DT DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DE Probable cysteine-rich antifungal protein LCR77 precursor (APP).
GN LCR77 OR A15G44420 OR MFCL6.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
NC1 _TaxID=3702;
RN (1)
RN RN SEQUENCE FROM N.A.
RP RC STRAIN=cv. Columbia;
RX MEDLINE=99397451; PubMed=10470850;
RA Kaneo T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.
RT Sequence features of the regions of 1,011,550 bp covered by seventeen
RT p1 and TAC clones."
RT DNA Res. 6:183-195(1999).
RN [2]
RN RN IDENTIFICATION.
RP RP Vancosthuyse V., Miesge C., Dumas C., Cock J.M.;
RA Submitted (JUN-2000) to Swiss-Brot.
RL -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the plant defensin family.
CC -----
CC CC

```

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CC or send an email to license@isb-sib.ch)

EMBL; AB017065; BAB09149.1; -.	
HSSR; P30231; IAYG.	
InterPro; IPR008176; Gamma-thionin.	
InterPro; IPR003614; Knc1.	
Pfam; PF00304; Gamma-thionin; 1.	
ProDom; PD002594; G_Purothionin; 1.	
SMART; SM00505; Knc1; 1.	
PROSITE; PS00940; GAMMA-THIONIN; 1.	
Plant defense; Fungicide; Signal; Multigene family;	
Pyrolidone carboxylic acid.	
SIGNAL	1 29
CHAIN	30 80
FT	POTENTIAL.
FT	PROBABLE CYSTEINE-RICH ANTIFUNGAL PROTEIN

```

FT  MOD_RES      30      30      PYRROLIDONE CARBOXYLIC ACID (BY
FT  DISULFID      33      80      SIMILARITY)
FT  DISULFID      44      65      BY SIMILARITY.
FT  DISULFID      50      74      BY SIMILARITY.
FT  DISULFID      54      76      BY SIMILARITY.
SQ  SEQUENCE      80 AA; 8518 MW; 2D0DAFB38E3B6321 CRC64;

Query Match      90.4%; Score 272; DB 1; Length 80;
Best Local Similarity 88.0%; Pred. No. 8.8e-24;
Matches 44; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy  1 KLCRSSGTWGVCGNNAKNCQIRLEGAGHGSNCNVVPPAHKICIVFPC 50
Db  31 KLCRKPSGTWGVCGNSACKNQCNINLEGAHGSNCNVVPPAHKICIVFPC 80

RESULT 12
AF2B SIGNAL
ID AF2B SIGNAL STANDARD; PRT; 52 AA.
AC Q10989;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 2B (AFP2B) (M2B).
OS Sinapis alba (White mustard) (Brassica hirta).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eucosids II; Brassicales; Brassicaceae; Sinapis.
OX NCBI_TaxID=3728;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RX MEDLINE=96433791; PubMed=8836771;
RA Neumann G.M., Condron R., Polya G.M.;
RT "Purification and mass spectrometry-based sequencing of yellow
RT mustard (Sinapis alba L.) 6 kDa proteins. Identification as
RT antifungal proteins."
RL Int. J. Pept. Protein Res. 47:437-446(1996).
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations.
CC -!- SUBUNIT: Forms oligomers in its native state.
CC -!- MASS SPECTROMETRY: MW=5840; MW ERR=1.2; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the plant defensin family.
DR HSP; P30231; IAYJ.
DR InterPro: IPR008176; Gamma-thionin.
DR Pfam: PF00304; Gamma-thionin; 1.
DR ProDom: PD002594; G-Purothionin; 1.
DR SMART: SM00505; Knot1; 1.
DR PROSITE: PS00940; GAMMA_THIONIN; FALSE NEG.
KW Fungicide; Pyrrolidone Carboxylic acid.
FT MOD_RES      4 1 PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
FT DISULFID      1 52 BY SIMILARITY.
FT DISULFID      16 37 BY SIMILARITY.
FT DISULFID      22 46 BY SIMILARITY.
FT DISULFID      26 48 BY SIMILARITY.
SQ SEQUENCE      52 AA; 5856 MW; A060FCBCL3A8D1FB CRC64;

Query Match      70.3%; Score 211.5; DB 1; Length 52;
Best Local Similarity 70.6%; Pred. No. 2.9e-17;
Matches 36; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Oy  1 KLCRSSGTW-GVCGNNAKNCQIRLEGAGHGSNCNVVPPAHKICIVFPC 50
Db  2 KLCARPSGTWSSGNCNNAKNCNFCIKLEKSRHGSNCNIPFNSKNCIVFPC 52

RESULT 13
ASFL_HELAN
ID ASFL_HELAN STANDARD; PRT; 161 AA.
AC P22357;

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DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Anther-specific protein SF18 precursor (Fragment).
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Asterales; Asteraceae; Heliantheae;
OC Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. HA401B / Cargill; TISSUE=Anther;
RX MEDLINE=9138702; PubMed=2102380;
RA Domon C., Eyraud J.-L., Herdenberger F., Pillay D.T.N., Steinmetz A.;
RT "Nucleotide sequence of two anther-specific cDNAs from sunflower
RT (Helianthus annuus L.).";
RL Plant Mol. Biol. 15:643-646(1990).
CC -!- FUNCTION: Anther-specific cell wall protein which could contribute
CC to the cell wall architecture of epidermal anther cells via
CC intermolecular disulfide bridges.
CC -!- TISSUE SPECIFICITY: Epidermal anther cells.
CC -!- DEVELOPMENTAL STAGE: Late developmental stages.
CC -!- SIMILARITY: Belongs to the plant defensin family.
CC -----
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CC -----
DR EMBL; X53375; CAA37455.1; -
DR PIR; S12246; S12246.
DR HSP; P30231; IAYJ.
DR InterPro: IPR008176; Gamma-thionin.
DR InterPro: IPR003614; Knot1.
DR Pfam: PF00304; Gamma-thionin; 1.
DR ProDom: PD002594; G-Purothionin; 1.
DR SMART: SM00505; Knot1; 1.
DR PROSITE: PS00940; GAMMA_THIONIN; 1.
KW Signal; Cell wall.
FT NON_TER      1 1
FT SIGNAL        1 8
FT CHAIN         9 161 ANTH-SPESIFIC PROTEIN SF18.
FT DOMAIN        9 65 GAMMA-THIONIN LIKE DOMAIN.
FT DOMAIN        70 161 PROLINE DOMAIN.
FT DISULFID      18 65 BY SIMILARITY.
FT DISULFID      29 50 BY SIMILARITY.
FT DISULFID      35 59 BY SIMILARITY.
FT DISULFID      39 61 BY SIMILARITY.
SQ SEQUENCE      161 AA; 15363 MW; 27A9CF4633ADA02B CRC64;

Query Match      48.2%; Score 145; DB 1; Length 161;
Best Local Similarity 46.0%; Pred. No. 1.9e-09;
Matches 23; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Oy  1 KLCRSSGTWGVCGNNAKNCQIRLEGAGHGSNCNVVPPAHKICIVFPC 50
Db  16 KICEKPSKTFWFGNCKDTCDCRCIDWEGAGHGHAKHGMFCYFDC 65

RESULT 14
AFPI_BRARA
ID AFPI_BRARA STANDARD; PRT; 27 AA.
AC P30227;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 1 (AFPI) (Fragment).
OS Brassica rapa (Turnip).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=51350;
 RN [1]
 RC SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=93138130; PubMed=8422949;
 RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RT Brassicaceae species."
 RL FEBS Lett. 316:233-240(1993).
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -!- SUBUNIT: Forms oligomers in its native state.
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 DR FIR; S28989; S28989.
 DR HSSP; P30231; 1AYJ.
 DR InterPro; IPR008176; Gamma-thionin.
 DR Pfam; PF003104; Gamma-thionin; 1.
 DR ProDom; PD002594; G_Purothionin; 1.
 DR PROSITE; PS00340; GAMMA_THIONIN; 1.
 KW Plant defense; Fungicide; Pyrrolidone carboxylic acid.
 FT MOD_RES 1
 FT NON_TER 27
 SQ SEQUENCE 27 AA; 2925 MW; 4C85BD9C611D4A9E CRC64;

Query Match 47.2%; Score 142; DS 1; Length 27;
 Best Local Similarity 96.0%; Pred. No. 7.6e-10;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KLCERSGTWSGVCNNACKNQCII 25
 |||||
 DB 2 KLCERPSTGTSVGCGNNACKNQCIR 26

RESULT 15

APP2_BRARA
 ID APP2_BRARA STANDARD; PRT; 27 AA.
 AC P30228;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 2 (APP2) (Fragment).
 OS Brassica rapa (turnip).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=51350;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=93138130; PubMed=8422949;
 RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RT Brassicaceae species."
 RL FEBS Lett. 316:233-240(1993).
 CC -!- FUNCTION: Possesses some antifungal activity sensitive to
 CC inorganic cations and antibacterial activity against B.megaterium.
 CC -!- SUBUNIT: Forms oligomers in its native state.
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 DR FIR; S28990; S28990.
 DR HSSP; P30231; 1AYJ.
 DR InterPro; IPR008176; Gamma-thionin.
 DR ProDom; PD002594; G_Purothionin; 1.
 DR PROSITE; PS00340; GAMMA_THIONIN; 1.
 KW Plant defense; Fungicide; Antibiotic; Pyrrolidone carboxylic acid.
 FT MOD_RES 1
 FT UNSURE 27
 FT NON_TER 27
 SQ SEQUENCE 27 AA; 2891 MW; 571E6D9C611D4A9E CRC64;

Query Match 44.5%; Score 134; DS 1; Length 27;
 Best Local Similarity 92.3%; Pred. No. 5.8e-09;
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 KLCERSGTWSGVCNNACKNQCII 26
 |||||
 DB 2 KLCERPSTGTSVGCGNNACKNQCIR 27

Search completed: May 11, 2004, 16:57:18
 Job time : 39 secs

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OM protein - protein search, using sw model

Run on: May 11, 2004, 16:53:44 ; Search time 39 Seconds
(without alignments)
404.511 Million cell updates/sec

Title: US-10-006-252A-10

Perfect score: 301

Sequence: 1 KLCERSSGTWSGCGNNAC.....QHGSNNYVPAHKICICYPC 50

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organella.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	284	94.4	80	10 Q94IN7	Q94IN7 brassica ol
2	283	94.0	80	10 Q8H6K0	Q8H6K0 brassica ra
3	279	92.7	80	10 Q9FS38	Q9FS38 eutrema was
4	272	90.4	80	10 Q9FI22	Q9FI22 arabidopsis
5	167	55.5	56	10 Q9FWR6	Q9FWR6 arabidopsis
6	167	55.5	78	10 Q8VZQ7	Q8VZQ7 arabidopsis
7	154	51.2	108	10 Q8LSM8	Q8LSM8 helianthus
8	129	42.9	132	10 Q84ZX5	Q84ZX5 artemisia v
9	116.5	38.7	80	10 Q9FZ31	Q9FZ31 arabidopsis
10	116.5	38.7	83	10 Q40779	Q40779 picea abies
11	115.5	38.4	83	10 Q8GTL2	Q8GTL2 picea abies
12	101.5	33.7	83	10 Q40539	Q40539 nicotiana t
13	86.5	28.7	77	10 P82788	P82788 arabidopsis
14	83.5	27.4	108	10 P82789	P82789 arabidopsis
15	82.5	27.4	105	10 Q40128	Q40128 lycopersico
16	81.5	27.1	81	10 Q948T2	Q948T2 pyrus pyrif

17	81.5	27.1	87	10 Q948T3	Q948T3 pyrus pyrif
18	81.5	27.1	87	10 Q948T4	Q948T4 pyrus pyrif
19	81.5	27.1	105	10 Q41105	Q41105 nicotiana e
20	81.5	27.1	559	5 Q9VZ44	Q9VZ44 drosophila
21	80.5	26.7	55	10 Q9C947	Q9C947 arabidopsis
22	80.5	26.7	76	10 Q8LEG6	Q8LEG6 arabidopsis
23	77.5	25.7	105	10 Q8GTMO	Q8GTMO nicotiana a
24	76.5	25.4	78	10 Q8W4V6	Q8W4V6 capsicum an
25	76.5	25.4	382	11 Q8K1E3	Q8K1E3 mus musculu
26	75.5	25.1	101	10 Q8H6Q0	Q8H6Q0 lytechinus
27	75.5	25.1	794	5 Q8T4P0	Q8T4P0 petunia hyb
28	75	24.9	85	5 Q7YXD3	Q7YXD3 androctonus
29	74.5	24.8	49	10 Q93WS9	Q93WS9 musa acumin
30	74	24.6	950	5 Q8MQN5	Q8MQN5 drosophila
31	74	24.6	1404	5 Q9VB65	Q9VB65 drosophila
32	73.5	24.4	584	5 Q8I498	Q8I498 cupienius
33	73.5	24.4	2233	5 Q94711	Q94711 paramesium ch
34	73	24.3	107	10 Q9XHE3	Q9XHE3 capsicum ch
35	72.5	24.1	129	10 Q8L8U0	Q8L8U0 arabidopsis
36	72.5	24.1	129	10 P82773	P82773 arabidopsis
37	72	23.9	721	13 Q7ZT69	Q7ZT69 lampetra ja
38	71.5	23.8	77	10 Q8H766	Q8H766 elaeis guin
39	71.5	23.8	78	10 Q8WB66	Q8WB66 nicotiana t
40	71.5	23.8	81	10 Q42225	Q42225 oryza sativ
41	70.5	23.4	72	10 Q9FR81	Q9FR81 prisma sativ
42	70.5	23.4	75	10 Q8W434	Q8W434 vigna radia
43	70.5	23.4	77	10 Q8LGD4	Q8LGD4 arabidopsis
44	70.5	23.4	78	10 Q8S8H3	Q8S8H3 arabidopsis
45	70.5	23.4	82	10 Q8L698	Q8L698 triticum ae

ALIGNMENTS

RESULT 1

Q94IN7	ID	Q94IN7	PRELIMINARY;	PRT;	80 AA.
AC	Q94IN7;				
DT	01-DEC-2001	(TrEMBLrel. 19, Created)			
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)			
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)			
DE	Defensin precursor.				
GN	Def.				
OS	Brassica oleracea (Cauliflower).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;				
OC	eurosid II; Brassicales; Brassicaceae; Brassica.				
OX	NCBI_TaxID=3712;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Benault R.;				
RT	"Brassica oleracea def gene for defensin.";				
RL	Submitted (APR-2001) to the EMBL/GenBank/DBSJ databases.				
DR	EMBL: AJ311046; CAC37558.1;				
GO	GO:0003793, P.defense/immunity protein activity; IEA.				
DR	InterPro: IPR008176; Gamma-thionin.				
DR	InterPro: IPR003614; Knott1.				
DR	Pfam: PF00304; Gamma-thionin; 1.				
DR	ProDom: PD002594; G Purothionin; 1.				
DR	SMART: SM00505; KncT1; 1.				
DR	PROSITE: PS00940; GAMMA_THIONIN; 1.				
KW	Signal.				
FT	SIGNAL				
SQ	SEQUENCE	80 AA; 8740 MW; 980477DFBD8D2690 CRC64;			
		1 29 POTENTIAL.			
		Query Match 94.4%; Score 284; DB 10; Length 80;			
		Best Local Similarity 94.0%; Pred. No. le-29;			
		Matches 47; Conservative 1; Mismatches 2; Indels 0; Gaps 0;			
QY	1	KLCERSSGTWSGCGNNACKQCIRLGAQHGSNNYVPAHKICICYPC 50			
Db	31	KLCERSSGTWSGCGNNACKQCIRLEKAREHGSNNYVPAHKICICYPC 80			

Query Match	92.7%;	Score 279;	DB 10;	Length 80;
Best Local Similarity	88.0%;	Pred. No. 4.6e-28;		
Matches 44;	Conservative 4;	Mismatches 2;	Indels 0;	Gaps
QY	1	KLCRSSGTSWGVCGNNNAKKNQCIIRLGAOHGSCNTVFFPAHKICICYPC	50	
DB	31	KLCRKSQTSWGVCGNNNAKKNQCNINLEGARHGSCNTVFFPHRCICYPC	80	
RESULT 4				
ID	Q9FI22	PRELIMINARY;	PRT;	80 AA.
ID	Q9FI22	AC		
DT	01-MAR-2001	(TrEMBLrel. 16, Created)		
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		
DE		Antifungal protein-like.		
OS		Arabidopsis thaliana (Mouse-ear cross).		
OC		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC		eurosids II; Brassicales; Brassicaceae; Arabidopsids.		
OX		NCBI_TaxID=3702;		
RN		[1]		
RC		SEQUENCE FROM N.A.		
RP		STRAIN=Columbia;		
RX		MEDLINE=99397451; PubMed=10470850;		
RA		Kaneko T., Katoh T., Sato S., Nakamura Y., Asanizu E., Kotani H.,		
RA		Miyajima N., Tabata S.;		
RT		"Structural analysis of Arabidopsis thaliana chromosome 5. IX.		
RT		Sequence features of the regions of 1,011,550 bp covered by seventeen		
RL		PI and TAC clones.";		
RL		DNA Res. 6,183-195(1999).		
DR		EMBL; AB037085; BAB09150.1; -.		
DR		HSP; F03031; IAPJ.		
DR		GO; GO:0003793; F:defense/immunity protein activity; IEA.		
DR		InterPro; IPR008176; Gamma-thionin.		
DR		InterPro; IPR003614; Knot1.		
DR		Pfam; PF00304; Gamma-thionin; 1.		
DR		ProDom; PD002594; G Purothionin; 1.		
DR		SMART; SM00505; Kncf1.1		
DR		PROSITE; PS00940; GAMMA_THIONIN; 1.		
SQ		SEQUENCE 80 AA; 8550 MW; 44ELFD8452AC76E CRG64;		
Query Match	90.4%;	Score 272;	DB 10;	Length 80;
Best Local Similarity	88.0%;	Pred. No. 3.9e-28;		
Matches 44;	Conservative 3;	Mismatches 3;	Indels 0;	Gaps
QY	1	KLCRSSGTSWGVCGNNNAKKNQCIIRLGAOHGSCNTVFFPAHKICICYPC	50	
DB	31	KLCRKSQTSWGVCGNNNAKKNQCNINLEGARHGSCNTVFFPAHKICICYPC	80	
RESULT 5				
ID	Q9FWR6	PRELIMINARY;	PRT;	56 AA.
ID	Q9FWR6	AC		
DT	01-MAR-2001	(TrEMBLrel. 16, Created)		
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		
DE		F14P1.6 protein.		
GN		F14P1.6		
OS		Arabidopsis thaliana (Mouse-ear cross).		
OC		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC		eurosids II; Brassicales; Brassicaceae; Arabidopsids.		
OX		NCBI_TaxID=3702;		
RN		[1]		
RP		SEQUENCE FROM N.A.		
RA		Rederspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,		
RA		Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,		
RA		Buehler E., Chao Q., Chin C., Chiu J., Choi E., Gonzalez A.,		
RA		Hwang B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,		

```
RA Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
RA Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC024609; AAF98402.1; -
DR PIR: G86328; G86328.
DR HSPF: F30231; IAU.
DR GO: GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro: IPR008176; Gamma-thionin.
DR Pfam: PF003614; Gamma-thionin.
DR ProDom: PD002594; G Purothionin; 1.
DR SMART: SM00505; KNOT1; 1.
DR PROSITE: PS00940; GAMMA_THIONIN; 1.
SQ SEQUENCE 56 AA; 6403 MW; 3BD56EAA25EBC442 CRC64;

Query Match 55.5%; Score 167; DB 10; Length 56;
Best Local Similarity 52.0%; Pred. No. 1.6e-14;
Matches 26; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 KLCRRSGTWSGVCNNACKNQCIRLEGAGHSCNYPFAHKICICYFPC 50
Db 7 RICERRSKTWTGFCGTRGCDSCQCKRWERASHGACHAQPFGFACFCYFNC 56

RESULT 6
QVZQ7 PRELIMINARY; PRT; 78 AA.
AC QVZQ7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative defensin AML1 protein.
GN At1g19610.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Ban J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene At1g19610 (GI:15223595).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Ban J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY063933; AAL36289.1; -
DR EMBL: AY114038; AAW45086.1; -
DR InterPro: IPR008176; Gamma-thionin.
DR Pfam: PF00304; Gamma-thionin; 1.
DR ProDom: PD002594; G Purothionin; 1.
DR PROSITE: PS00940; GAMMA_THIONIN; 1.
SQ SEQUENCE 78 AA; 8840 MW; A5B5DD28303A6545 CRC64;

Query Match 55.5%; Score 167; DB 10; Length 78;
Best Local Similarity 52.0%; Pred. No. 2.2e-14;
Matches 26; Conservative 6; Mismatches 18; Indels 0; Gaps 0;
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QY 1 KLCRRSGTWSGVCNNACKNQCIRLEGAGHSCNYPFAHKICICYFPC 50
Db 29 RICERRSKTWTGFCGTRGCDSCQCKRWERASHGACHAQPFGFACFCYFNC 78

RESULT 7
Q8LSM8 PRELIMINARY; PRT; 108 AA.
AC Q8LSM8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Defensin.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Asteraceae; Heliantheae;
OC Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RA Hu X., Bidney D., Duvick J., Yalpani N., Crasta O., Folkerts O.,
RA Lu G.;
RT "Oxalate oxidase confers Sclerotinia resistance.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF364865; AAM27914.1; -
DR GO: GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro: IPR008176; Gamma-thionin.
DR InterPro: IPR003614; KNOT1.
DR Pfam: PF00304; Gamma-thionin; 1.
DR ProDom: PD002594; G Purothionin; 1.
DR SMART: SM00505; KNOT1; 1.
SQ SEQUENCE 108 AA; 11866 MW; 631ECD8F02F21AD0 CRC64;

Query Match 51.2%; Score 154; DB 10; Length 108;
Best Local Similarity 50.0%; Pred. No. 1.5e-12;
Matches 25; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 KLCRRSGTWSGVCNNACKNQCIRLEGAGHSCNYPFAHKICICYFPC 50
Db 29 ELCEKASQTWSGTCGKTKHCDCKSWEGAHGACHVDRGKEMCFCYFNC 78

RESULT 8
Q84ZX5 PRELIMINARY; PRT; 132 AA.
AC Q84ZX5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Major pollen allergen Art v 1 precursor.
OS Artemisia vulgaris (Mugwort).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Asteraceae; Anthemideae;
OC Artemisia.
OX NCBI_TaxID=4220;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pollen;
EX MEDLINE=22409970; PubMed=12475905;
RA Himly M., Jahn-Schmid B., Dedic A., Kelemen P., Wopfner N.,
RA Altman F., van Ree R., Briza P., Richter K., Ebner C., Ferreira F.;
RT "Art v 1, the major allergen of mugwort pollen, is a modular
glycoprotein with a defensin-like and a hydroxyproline-rich domain.";
RL FASEB J. 17:106-108(2003).
DR EMBL: AF493943; AAC24900.1; -
DR GO: GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro: IPR008176; Gamma-thionin.
DR InterPro: IPR003614; KNOT1.
DR Pfam: PF00304; Gamma-thionin; 1.
DR SMART: SM00505; KNOT1; 1.
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KW Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 132 MAJOR POLLEN ALLERGEN ART V 1.
SQ SEQUENCE 132 AA; 13404 MW; 745249C89919F316 CRC64;
Query Match 42.9%; Score 129; DB 10; Length 132;
Best Local Similarity 45.6%; Pred. No. 3.6e-09;
Matches 26; Conservative 6; Mismatches 11; Indels 14; Gaps 3;
QY 1 KLCRSSGTWGVCGNNACKNQCIRLEGAQHGSQNYVFPAAHK-----CICYPFC 50
DB 28 KLCBKTSTSGKC-DNKKCKXKEWKAQHGC-----HKREAGKSCFCYFDC 77
RESULT 9
Q3FZ31 PRELIMINARY; PRT; 80 AA.
ID Q9FZ31
AC Q9FZ31
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative antifungal protein (Cysteine-rich antifungal protein,
putative).
GN T24C10.12 OR F14C21.57.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Alfafri H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
RA Buehler E., Chao Q., Chin C., Chiu J., Choi E., Gonzalez A.,
RA Howing B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
RA Lenz C., Liu A., Liu S., Mukharshy N., Pham P., Sakano H., Shinn P.,
RA Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altai H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egtu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizari L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hopfer S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana."
RL Nature 408:816-820(2000).
DR EMBL; AC064840; AAG00880.1; -
DR EMBL; AC069144; AAG51104.1; -
DR FIR; F96591; F96591.
DR HSP; P30231; 1AYJ.
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR008176; Gamma-thionin.
DR Pfam; PF003614; Knott1.
DR ProDom; PD002594; G_Purothionin; 1.
DR SMART; SM00505; KncF1; 1.
SQ SEQUENCE 80 AA; 9139 MW; 8E9BF4ACA794071 CRC64;

Query Match 38.7%; Score 116.5; DB 10; Length 80;
Best Local Similarity 39.2%; Pred. No. 9.6e-08;
Matches 20; Conservative 10; Mismatches 20; Indels 1; Gaps 1;
QY 1 KLCRSSGTWGVCGNNACKNQCIRLEGAQHGSQNYVFPAAHK-CICYPFC 50
DB 30 ELCKRESEWGRVNDYQCRDHCINNRDNGDYGAGYFWYSCFFFC 80
RESULT 10
Q40779 PRELIMINARY; PRT; 83 AA.
ID Q40779
AC Q40779
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative gamma-thionin protein precursor.
GN SP11.
OS Picea abies (Norway spruce) (Picea excelsa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3329;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root;
RA Sharma P., Linneberg A.;
RT "Isolation and characterization of a cDNA encoding a gamma-thionin-
like protein from roots of Norway spruce."
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X91487; CAA62761.1; -
DR PIR; T14866; T14866.
DR HSP; P41964; 1MYN.
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR008176; Gamma-thionin.
DR InterPro; IPR003614; Knott1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.
DR SMART; SM00505; KncF1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
KW Signal.
FT SIGNAL 1 32 POTENTIAL.
SQ SEQUENCE 83 AA; 8835 MW; B94207ADAB8FE4A5 CRC64;
Query Match 38.7%; Score 116.5; DB 10; Length 83;
Best Local Similarity 42.0%; Pred. No. 9.9e-08;
Matches 21; Conservative 8; Mismatches 20; Indels 1; Gaps 1;
QY 1 KLCRSSGTWGVCGNNACKNQCIRLEGAQHGSQNYVFPAAHK-CICYPFC 50
DB 34 RTCKTPSGKFKGVCASSNNCKNVC-QTEGFPSSGCDFFHVRKCYCKPC 82
RESULT 11
Q8GTL2 PRELIMINARY; PRT; 83 AA.
ID Q8GTL2
AC Q8GTL2
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative plant defensin SP11b.
OS Picea abies (Norway spruce) (Picea excelsa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3329;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Needle;
RA Fosdal C.G.;
RT "The putative gymnosperm plant defensin (SP11) accumulates after seed
germination and a related SP11b cDNA is found in needles."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF548021; AAN40688.1; -
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.


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DR InterPro: IPR008176; Gamma-thionin.
DR InterPro: IPR003614; Knot1.
DR Pfam: PF00304; Gamma-thionin; 1.
DR ProDom: PD002594; G Purothionin; 1.
DR SMART: SM00505; Knot1; 1.
DR PROSITE: PS00940; GAMMA THIONIN; 1.
SQ SEQUENCE 83 AA; 8888 MW; E45BF9561B9AA3D2 CRC64;

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Best Local Similarity 42.0%; Pred. No. 1.3e-07;
Matches 21; Conservative 7; Mismatches 21; Indels 1; Gaps 1;

Qy 1 KLCERSSTGWSGVCNNACKQCIRLEGAHQSCNVVFPFAHKICICYFPC 50
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AC Q40539;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pti1 protein.
GN Pti1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
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RN SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RC MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Barnstead M.E., Feldblyum T.V.,
RA Fujii C.R., Mason T.M., Bowman C.L., Bowning C.M., Koo H., Moffat K.S.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon L.J., Gill J.E.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Coppenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP IDENTIFICATION.
RX PubMed=11437247;
RA Vancosthuyse V., Mielge C., Dumas C., Cock J.M.;
RT "Two large Arabidopsis thaliana gene families are homologous to the
RT Brassica gene superfamily that encodes pollen coat proteins and the
RT male component of the self-incompatibility response.";
RL Plant Mol. Biol. 46:17-34(2001).
CC -1- SIMILARITY: BELONGS TO THE PLANT DEFENSIN FAMILY.
DR EMBL; AC006223; -; NOT ANNOTATED CDS.
DR InterPro: IPR008176; Gamma-thionin.
DR Pfam: PF00304; Gamma-thionin; 1.
DR ProDom: PD002594; G Purothionin; 1.
DR PROSITE; PS00940; GAMMA THIONIN; FALSE NEG.
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FT CHAIN 25 77 HYPOTHETICAL PROTEIN LCR79.
FT DISULFID 28 72 BY SIMILARITY.
FT DISULFID 39 59 BY SIMILARITY.
FT DISULFID 45 66 BY SIMILARITY.
FT DISULFID 49 68 BY SIMILARITY.
SQ SEQUENCE 77 AA; 8909 MW; 97194D61E5620DBE CRC64;

Query Match 28.7%; Score 86.5; DB 10; Length 77;
Best Local Similarity 38.0%; Pred. No. 0.0008;
Matches 19; Conservative 4; Mismatches 24; Indels 3; Gaps 2;

Qy 1 KLCERSSTGWSGVCNNACKQCIRLEGAHQSCNVVFPFAHKICICYFPC 50
Db 26 QMCEAKSLDWKMLKWRNCRQVCIS-EGFTDGRCKGF--TRKICCRKPC 72

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ID P82789
AC P82789;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein LCR80 precursor.
GN LCR80.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=98344145; PubMed=9679202;
RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
RT features of the regions of 1,361,565 bp covered by twenty one
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:131-145(1998).
RN [2]
RP IDENTIFICATION.
RX PubMed=11437247;

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RN SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RC MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Barnstead M.E., Feldblyum T.V.,
RA Fujii C.R., Mason T.M., Bowman C.L., Bowning C.M., Koo H., Moffat K.S.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon L.J., Gill J.E.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Coppenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP IDENTIFICATION.
RX PubMed=11437247;
RA Vancosthuyse V., Mielge C., Dumas C., Cock J.M.;
RT "Two large Arabidopsis thaliana gene families are homologous to the
RT Brassica gene superfamily that encodes pollen coat proteins and the
RT male component of the self-incompatibility response.";
RL Plant Mol. Biol. 46:17-34(2001).
CC -1- SIMILARITY: BELONGS TO THE PLANT DEFENSIN FAMILY.
DR EMBL; AC006223; -; NOT ANNOTATED CDS.
DR InterPro: IPR008176; Gamma-thionin.
DR Pfam: PF00304; Gamma-thionin; 1.
DR ProDom: PD002594; G Purothionin; 1.
DR PROSITE; PS00940; GAMMA THIONIN; FALSE NEG.
KW Hypothetical protein; Signal; Plant defense.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 77 HYPOTHETICAL PROTEIN LCR79.
FT DISULFID 28 72 BY SIMILARITY.
FT DISULFID 39 59 BY SIMILARITY.
FT DISULFID 45 66 BY SIMILARITY.
FT DISULFID 49 68 BY SIMILARITY.
SQ SEQUENCE 77 AA; 8909 MW; 97194D61E5620DBE CRC64;

Query Match 28.7%; Score 86.5; DB 10; Length 77;
Best Local Similarity 38.0%; Pred. No. 0.0008;
Matches 19; Conservative 4; Mismatches 24; Indels 3; Gaps 2;

Qy 1 KLCERSSTGWSGVCNNACKQCIRLEGAHQSCNVVFPFAHKICICYFPC 50
Db 26 QMCEAKSLDWKMLKWRNCRQVCIS-EGFTDGRCKGF--TRKICCRKPC 72

RESULT 14
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ID P82789
AC P82789;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein LCR80 precursor.
GN LCR80.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=98344145; PubMed=9679202;
RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
RT features of the regions of 1,361,565 bp covered by twenty one
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:131-145(1998).
RN [2]
RP IDENTIFICATION.
RX PubMed=11437247;

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RA Vanoosthuyse V., Mies C., Dumas C., Cock J.M.;
RT "Two large Arabidopsis thaliana gene families are homologous to the
RT Brassica gene superfamily that encodes pollen coat proteins and the
RT male component of the self-incompatibility response.";
RL Plant Mol. Biol. 46:17-34(2001).
DR EMBL: AB011481; -; NOT ANNOTATED CDS.
DR GO: GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR003614; Knot1.
DR SMART; SM00505; Knot1; 1.
DR Hypothetical protein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 108 HYPOTHETICAL PROTEIN LCR80.
SQ SEQUENCE 108 AA; 11551 MW; 11E28E2CEB3578A7 CRC64;

Query Match 27.7%; Score 83.5; DB 10; Length 108;
Best Local Similarity 32.0%; Pred. No. 0.0027; Indels 1; Gaps 1;
Matches 16; Conservative 4; Mismatches 29;

Qy 1 KLCERSGTSWGVCGNNACKNCICIRLEGAQHGSNCYVFPAAHKICICYPPC 50
Db 60 KLCNGGLGCGESC-NEQCDCRNCQRYNGHGYCNTLDDFSLCLCKYPC 108

RESULT 15
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AC Q00128;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Flower-specific gamma-thionin-like protein/acidic protein
DE precursor.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF36; TISSUE=Pistil;
RX MEDLINE=95375233; PubMed=7647301;
RA Milligan S.B., Gasser C.S.;
RT "Nature and regulation of pistil-expressed genes in tomato.";
RL Plant Mol. Biol. 28:691-711(1995).
DR EMBL: U20591; AAA80496.1; -.
DR PIR: S57809.
DR GO: GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR008176; Gamma-thionin.
DR InterPro; IPR003614; Knot1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD02594; G Purothionin; 1.
DR SMART; SM00505; Knot1; 1.
KW Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 73 GAMMA-THIONIN-LIKE PROTEIN.
FT CHAIN 74 105 ACIDIC PROTEIN.
SQ SEQUENCE 105 AA; 11914 MW; ADC9B7ECB620E814 CRC64;

Query Match 27.4%; Score 82.5; DB 10; Length 105;
Best Local Similarity 32.0%; Pred. No. 0.0036; Indels 3; Gaps 2;
Matches 16; Conservative 13; Mismatches 18;

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Db 27 QICKAPSQTPPGLCFMDSSCKYCIK-EKFTGGHCSKL--QRKCLCTRKC 73

Search completed: May 11, 2004, 16:57:46
Job time : 41 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 13, 2004, 10:11:08 ; Search time 1734 Seconds
(without alignments)
1249.799 Million cell updates/sec

Title: US-10-006-252a-10
Perfect score: 301
Sequence: 1 KLCRSSGTSWGVCGNNAC.....QHGSNCYVFAHKICICYFPC 50

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q/cn2 1/USPTO spoel p/US10006252/runat 11052004.141947.10947/app_query.fasta_1.199
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -NORM=ext -HRAPISE=500 -MINLEN=0 -MAXLEN=2000000000
-OUTFMT=ptc -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NO MMAP -LARGEQUERY -WARM TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	301	100.0	475	8	RSEFP3
3	284	94.4	933	8	BOL311046
4	283	94.0	363	8	AF528180
5	282	93.7	499	8	RGAFF4
6	281	93.4	285	6	AR014693
7	281	93.4	285	6	AR432393
8	281	93.4	288	6	AR5553
9	281	93.4	288	6	AR050161
10	281	93.4	288	6	AR130280
11	281	93.4	288	6	I23736
12	281	93.4	308	6	AR014682
13	281	93.4	308	6	AR432382
14	281	93.4	449	6	E34290
15	281	93.4	457	8	RSU18556
16	281	93.4	522	6	BD223233
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18	281	93.4	534	6	BD223234
19	281	93.4	534	6	BD223237
20	281	93.4	606	6	BD223236
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29	279	92.7	414	6	AR130272
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34	279	92.7	414	8	ABO12871
35	279	92.7	497	11	BV010712
36	279	92.7	541	11	BV010697
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43	274	91.0	403	6	A68645
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ALIGNMENTS

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VERSION U59459.1 GI:1399229
KEYWORDS
SOURCE Brassica napus (rape)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 451)
AUTHORS Sohn,U., Lee,C.M., Lee,M.H. and Kim,J.H.
TITLE Brassica napus cDNAs
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 451)
AUTHORS Sohn,U., Lee,C.M., Lee,M.H. and Kim,J.H.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-1996) Department of Genetic Engineering,
Kyungpook National University, Puk-Ku, Sankyuk-Dong 1370, Taegu
702-701, Korea
COMMENT On Jul 1, 1996 this sequence version replaced gi:12933377.
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DB 173 AAGATCAGTGCATTCGACTTGAAGGAGCACAACTGATCATGCACTATGTGTTCCCT 232
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VERSION X97319.1 GI:1655684
KEYWORDS AFP; antifungal protein 3.
SOURCE Raphanus sativus (radish)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.

1
REFERENCE Terras,F.R.G., Goderis,I.J., Penninckx,I.J., Osborn,R.W. and
AUTHORS Broeksart,W.F.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 475)
AUTHORS Terras,F.R.G.
TITLE Direct Submission
JOURNAL Submitted (09-APR-1996) F.R.G. Terras, Institut fur
Pflanzenbiochemie, Stress- und Entwicklungsbiologie, Weinberg 3,
Halle (Saale), D-06120, FRG
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QY 21 LysAsnGlnCysIleArgLeuGlnGlyAlaGlnHisGlySerCysAsnTyValPhePro 40
DB 175 AAGATCAGTGCATTCGACTTGAAGGAGCACAACTGATCTTGCAACTATGTGTTCCCT 234
QY 41 AlaHisLysCysIleCysTyPheProCys 50
DB 235 GCTCACAAGTGTATCTGCTATTTCCCATGT 264
RESULT 3
BOL311046
LOCUS BOL311046 933 bp DNA linear PLN 26-APR-2001
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ACCESSION AJ311046
VERSION AJ311046.1 GI:13872713
KEYWORDS def gene; defensin.
SOURCE Brassica oleracea
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1
AUTHORS Esnault,R.

TITLE
JOURNAL Brassica oleracea def gene for defensin
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 933)
TITLE Esnault, R.
JOURNAL Direct Submission
 Submitted (24-APR-2001) Esnault R., Institut des Sciences
 Vegetales, C.N.R.S., Avenue de la Terrasse, 91 198 Gif sur Yvette
 cedex, FRANCE

FEATURES
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 /product="defensin"
 /protein_id="CAC37558.1"
 /db_xref="GI:13872714"
 /db_xref="GOA:Q94IN7"
 /db_xref="SPTREMBL:Q94IN7"
 /translation="MAKVASIVALLFPALVIFPAFEAPTWVAQKLCERPSTWSGVC
 GNNACKNQICRLKRGHSCNVYFPARHCICYPFC"
 join(366..429,528..550)
 /gene="def"
 366..429
 /gene="def"
 430..527
 /gene="def"
 /number=1
 528..5706
 /gene="def"
 /number=2
 824..829
 /gene="def"

sig_peptide
 1..363
 /note="induced by Pseudomonas syringae pv. tomato"
 /codon_start=1
 /product="defensin"
 /protein_id="AAN23105.1"
 /db_xref="GI:23321205"
 /translation="MAKFAVSIITLFFAALVLPFAFEAPTWVAQKLCERSSTGWSGVC
 GNNACKNQICRLKRGHSCNVYFPARHCICYPFC"

exon
 1..363
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="mRNA"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 22..264
 /note="induced by Pseudomonas syringae pv. tomato"
 /codon_start=1
 /product="defensin"
 /protein_id="AAN23105.1"
 /db_xref="GI:23321205"
 /translation="MAKFAVSIITLFFAALVLPFAFEAPTWVAQKLCERSSTGWSGVC
 GNNACKNQICRLKRGHSCNVYFPARHCICYPFC"

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 363..46
 /note="induced by Pseudomonas syringae pv. tomato"
 /codon_start=1
 /product="defensin"
 /protein_id="AAN23105.1"
 /db_xref="GI:23321205"
 /translation="MAKFAVSIITLFFAALVLPFAFEAPTWVAQKLCERSSTGWSGVC
 GNNACKNQICRLKRGHSCNVYFPARHCICYPFC"

exon
 46..2
 /note="induced by Pseudomonas syringae pv. tomato"
 /codon_start=1
 /product="defensin"
 /protein_id="AAN23105.1"
 /db_xref="GI:23321205"
 /translation="MAKFAVSIITLFFAALVLPFAFEAPTWVAQKLCERSSTGWSGVC
 GNNACKNQICRLKRGHSCNVYFPARHCICYPFC"

polya_signal
 261..50
 /note="induced by Pseudomonas syringae pv. tomato"
 /codon_start=1
 /product="defensin"
 /protein_id="AAN23105.1"
 /db_xref="GI:23321205"
 /translation="MAKFAVSIITLFFAALVLPFAFEAPTWVAQKLCERSSTGWSGVC
 GNNACKNQICRLKRGHSCNVYFPARHCICYPFC"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.76e-27 Length: 363
 Score: 283.00 Matches: 46
 Percent Similarity: 95.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 94.02% Indels: 0
 DB: 8 Gaps: 0
 US-10-006-252A-10 (1-50) x AF528180 (1-363)

QY 1 LysLeuCysGluArgSerSerglyThrTrpSerglyValCysGlyAsnAsnAlaCys 20
 Db 112 AAGTTGTGCGAGAGGTCTAGTGGACATGGTCAGAGTATGTGGAAATAACAATGCTTGC 171
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 172 AAGAACCAAGTGCATCACTTGGAGGACGACATGATCTTGCACACTATGTTTCCCA 231
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 232 TATCACAGGTGATCTGCTACTTCCCATGT 261

RESULT 5
 RSAPP4
 LOCUS
 DEFINITION R. sativus mRNA for antifungal protein 4.
 ACCESSION X97318
 VERSION X97318.1 GI:1655682
 KEYWORDS APP; antifungal protein 4.
 SOURCE Raphanus sativus (radish)
 ORGANISM Raphanus sativus
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
 Terras, F.R.G., Godeis, I.J., Penninckx, I.J., Osborn, R.W. and
 Broekaert, W.F.
 Unpublished

RESULT 4
 AF528180
 LOCUS
 DEFINITION Brassica rapa subsp. pekinensis defensin mRNA, complete cds.
 ACCESSION AF528180
 VERSION AF528180.1 GI:23321204
 KEYWORDS
 ORGANISM Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 Ryang, S.-H., Chung, S.-Y., Park, Y.-S. and Cho, T.-J.
 Characterization of Chinese cabbage genes induced by Pseudomonas
 syringae pv. tomato
 Unpublished
 2 (bases 1 to 363)
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="mRNA"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 22..264
 /note="induced by Pseudomonas syringae pv. tomato"
 /codon_start=1
 /product="defensin"
 /protein_id="AAN23105.1"
 /db_xref="GI:23321205"
 /translation="MAKFAVSIITLFFAALVLPFAFEAPTWVAQKLCERSSTGWSGVC
 GNNACKNQICRLKRGHSCNVYFPARHCICYPFC"

RESULT 5
 RSAPP4
 LOCUS
 DEFINITION R. sativus mRNA for antifungal protein 4.
 ACCESSION X97318
 VERSION X97318.1 GI:1655682
 KEYWORDS APP; antifungal protein 4.
 SOURCE Raphanus sativus (radish)
 ORGANISM Raphanus sativus
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
 Terras, F.R.G., Godeis, I.J., Penninckx, I.J., Osborn, R.W. and
 Broekaert, W.F.
 Unpublished

REFERENCE 2 (bases 1 to 499)
 AUTHORS Terras, F.R.G.
 TITLE Direct Submission
 JOURNAL Submitted (09-APR-1996) F.R.G. Terras, Institut fur Pflanzenbiochemie, Stress- und Entwicklungsbiologie, Weinberg 3, Halle (Saale), D-06120, FRG

FEATURES
 source
 1..499
 Location/Qualifiers
 /organism="Raphanus sativus"
 /mol_type="mRNA"
 /culturvar="Ronde Rode Kleine Witpunt"
 /db_xref="taxon:3728"
 /dev_stage="adult plants infected with Alternaria brassicicola"
 gene
 1..499
 /gene="AFP"
 CDS
 44..286
 /gene="AFP"
 /codon_start=1
 /product="antifungal protein 4"
 /protein_id="CAA65983.1"
 /db_xref="GI:1655683"
 /db_xref="GOA:O24331"
 /db_xref="SWISS-PROT:O24331"
 /translation="MAKFSVLIITLLEVALVLEPAEPTWVEAQKLCERSSGTWSGVC
 GNNACKNQINLEGARHGSNFIFFHRCICFFPC"
 sig_peptide
 44..130
 /gene="AFP"
 mat_peptide
 131..283
 /gene="AFP"
 /product="antifungal protein 4"

ORIGIN
 Alignment Scores:
 Pred. No.: 3,37e-27 Length: 499
 Score: 282.00 Matches: 45
 Percent Similarity: 96.00% Conservative: 3
 Best Local Similarity: 90.00% Mismatches: 2
 Query Match: 93.69% Indels: 0
 DB: 8 Gaps: 0

US-10-006-252A-10 (1-50) x RSAPP4 (1-499)

QY 1 LysLeuCysGluArgSerGlyThrTpsSerGlyValCysGlyValAsnAsnAlaCys 20
 Db 134 AAGTTGGCGAGAGCTCTAGTGGACATGTCAGGATGATGGAAATAATGCTTGC 193

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 194 AAGAACCAGTGCATCAACCTCGAGGGAGCAGCATGATCTTGCACTATATTTCCCA 253

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 254 TATCACAGGTGATCTGCTACTTCCCATGT 283

RESULT 6
 AR014693
 LOCUS AR014693 285 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 17 from patent US 5773696.
 ACCESSION AR014693
 VERSION AR014693.1 GI:3972147
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 285)
 AUTHORS Liang, J., Shan, D., Maganlal., Wu, Y., Shun. and Rosenberger, C. Annette.
 TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
 JOURNAL Patent: US 5773696-A 17 30-JUN-1998;
 FEATURES Location/Qualifiers
 source
 1..285
 /organism="unknown"

ORIGIN /mol_type="unassigned DNA"

Alignment Scores:
 Pred. No.: 2,44e-27 Length: 285
 Score: 281.00 Matches: 46
 Percent Similarity: 96.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 6 Gaps: 0

US-10-006-252A-10 (1-50) x AR014693 (1-285)

QY 1 LysLeuCysGluArgSerGlyThrTpsSerGlyValCysGlyValAsnAsnAlaCys 20
 Db 121 AAGTTGGCGCAAGGCCATCAGGGACTTGGTCAGAGTCTGCGGAAACAACAACGCGATGC 180

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 181 AAGAACCAGTGCATCAGACTCGAGAAGGCAAGCATGATCTTGCACTACGTCTTCCCA 240

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 241 GCTCACAGTGCATCTGCTACTTTCATGC 270

RESULT 7
 AR432393
 LOCUS AR432393 285 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 17 from patent US 6653280.
 ACCESSION AR432393
 VERSION AR432393.1 GI:40194670
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 285)
 AUTHORS Liang, J., Shan, D.M., Wu, Y.S. and Rosenberger, C.A.
 TITLE Antifungal polypeptide AlyAPP from Alyssum and methods for controlling plant pathogenic fungi
 JOURNAL Patent: US 6653280-A 17 25-NOV-2003;
 FEATURES Location/Qualifiers
 source
 1..285
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN /mol_type="unassigned DNA"

Alignment Scores:
 Pred. No.: 2,44e-27 Length: 285
 Score: 281.00 Matches: 46
 Percent Similarity: 96.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 6 Gaps: 0

US-10-006-252A-10 (1-50) x AR432393 (1-285)

QY 1 LysLeuCysGluArgSerGlyThrTpsSerGlyValCysGlyValAsnAsnAlaCys 20
 Db 121 AAGTTGGCGCAAGGCCATCAGGGACTTGGTCAGAGTCTGCGGAAACAACAACGCGATGC 180

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 181 AAGAACCAGTGCATCAGACTCGAGAAGGCAAGCATGATCTTGCACTACGTCTTCCCA 240

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 241 GCTCACAGTGCATCTGCTACTTTCATGC 270

RESULT 8
 A39553
 LOCUS A39553 288 bp DNA linear PAT 05-MAR-1997
 DEFINITION Sequence 41 from Patent WO9416076.
 ACCESSION A39553

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VERSION      A39553.1  GI:2295844
KEYWORDS
SOURCE       unidentified
ORGANISM     unidentified
REFERENCE    1 (bases 1 to 288)
AUTHORS      Dubock,A.C., Powell,K.A. and Rees,S.B.
TITLE        ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
JOURNAL      ZENECA LTD (GB)
COMMENT      Other publication AU 5820494 940815.
FEATURES
  source     Location/Qualifiers
            1..288
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

ORIGIN
Alignment Scores:
  Pred. No.:      2.47e-27      Length:      288
  Score:          281.00        Matches:    46
  Percent Similarity: 96.00%    Conservative: 2
  Best Local Similarity: 92.00% Mismatches: 2
  Query Match:    93.36%       Indels:    0
  DB:             Gaps:       0

US-10-006-252A-10 (1-50) x A39553 (1-288)

QY      1  LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
      133  AAGTTGTGCCAAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
      193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGCTTCCCA 252

QY      41  AlaHisLysCysIleCysTyrPheProCys 50
      253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

QY      1  LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
      133  AAGTTGTGCCAAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
      193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGCTTCCCA 252

QY      41  AlaHisLysCysIleCysTyrPheProCys 50
      253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

RESULT 9
AR050161
LOCUS       AR050161
DEFINITION Sequence 58 from patent US 5824869.
ACCESSION  AR050161
VERSION     AR050161.1  GI:5972153
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unassigned.
REFERENCE    1 (bases 1 to 288)
AUTHORS      Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
              Terras,F.R.G. and Vanderleyden,J.
TITLE        Biocidal proteins
JOURNAL      Patent: US 5824869-A 58 20-OCT-1998;
              Location/Qualifiers
              source     1..288
              /organism="unassigned DNA"
              /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
  Pred. No.:      2.47e-27      Length:      288
  Score:          281.00        Matches:    46
  Percent Similarity: 96.00%    Conservative: 2
  Best Local Similarity: 92.00% Mismatches: 2
  Query Match:    93.36%       Indels:    0
  DB:             Gaps:       0

US-10-006-252A-10 (1-50) x AR050161 (1-288)

QY      1  LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
      133  AAGTTGTGCCAAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
      193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGCTTCCCA 252

QY      41  AlaHisLysCysIleCysTyrPheProCys 50
      253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

RESULT 11
AR050161
LOCUS       AR050161
DEFINITION Sequence 58 from patent US 5538525.
ACCESSION  AR050161
VERSION     AR050161.1  GI:1603606
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unassigned.
REFERENCE    1 (bases 1 to 288)
AUTHORS      Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
              Terras,F.R.G. and Vanderleyden,J.
TITLE        Biocidal proteins
JOURNAL      Patent: US 5538525-A 58 23-JUL-1996;
              Location/Qualifiers
              source     1..288
              /organism="unassigned DNA"
              /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
  Pred. No.:      2.47e-27      Length:      288
  Score:          281.00        Matches:    46
  Percent Similarity: 96.00%    Conservative: 2
  Best Local Similarity: 92.00% Mismatches: 2
  Query Match:    93.36%       Indels:    0
  DB:             Gaps:       0

US-10-006-252A-10 (1-50) x AR050161 (1-288)

QY      1  LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
      133  AAGTTGTGCCAAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
      193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGCTTCCCA 252

QY      41  AlaHisLysCysIleCysTyrPheProCys 50
      253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

RESULT 10
AR130280
LOCUS       AR130280
DEFINITION Sequence 58 from patent US 6187904.
ACCESSION  AR130280
VERSION     AR130280.1  GI:14118177
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unassigned.
REFERENCE    1 (bases 1 to 288)
AUTHORS      Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
              Terras,F.R.G. and Vanderleyden,J.
TITLE        Biocidal proteins
JOURNAL      Patent: US 6187904-A 58 13-FEB-2001;
              Location/Qualifiers
              source     1..288
              /organism="unassigned DNA"
              /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
  Pred. No.:      2.47e-27      Length:      288
  Score:          281.00        Matches:    46
  Percent Similarity: 96.00%    Conservative: 2
  Best Local Similarity: 92.00% Mismatches: 2
  Query Match:    93.36%       Indels:    0
  DB:             Gaps:       0

US-10-006-252A-10 (1-50) x AR130280 (1-288)

QY      1  LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
      133  AAGTTGTGCCAAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
      193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGCTTCCCA 252

QY      41  AlaHisLysCysIleCysTyrPheProCys 50
      253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

RESULT 11
AR130280
LOCUS       AR130280
DEFINITION Sequence 58 from patent US 5538525.
ACCESSION  AR130280
VERSION     AR130280.1  GI:1603606
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unassigned.
REFERENCE    1 (bases 1 to 288)
AUTHORS      Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
              Terras,F.R.G. and Vanderleyden,J.
TITLE        Biocidal proteins
JOURNAL      Patent: US 5538525-A 58 23-JUL-1996;
              Location/Qualifiers
              source     1..288
              /organism="unassigned DNA"
              /mol_type="unassigned DNA"

ORIGIN

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Db      133  AAGTTGTGCCAAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
      193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGCTTCCCA 252

QY      41  AlaHisLysCysIleCysTyrPheProCys 50
      253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

Db      133  AAGTTGTGCCAAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
      193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGCTTCCCA 252

QY      41  AlaHisLysCysIleCysTyrPheProCys 50
      253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

RESULT 10
AR130280
LOCUS       AR130280
DEFINITION Sequence 58 from patent US 6187904.
ACCESSION  AR130280
VERSION     AR130280.1  GI:14118177
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unassigned.
REFERENCE    1 (bases 1 to 288)
AUTHORS      Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
              Terras,F.R.G. and Vanderleyden,J.
TITLE        Biocidal proteins
JOURNAL      Patent: US 6187904-A 58 13-FEB-2001;
              Location/Qualifiers
              source     1..288
              /organism="unassigned DNA"
              /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
  Pred. No.:      2.47e-27      Length:      288
  Score:          281.00        Matches:    46
  Percent Similarity: 96.00%    Conservative: 2
  Best Local Similarity: 92.00% Mismatches: 2
  Query Match:    93.36%       Indels:    0
  DB:             Gaps:       0

US-10-006-252A-10 (1-50) x AR130280 (1-288)

QY      1  LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
      133  AAGTTGTGCCAAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACATAACGCATGC 192

QY      21  LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
      193  AAGAATCAGTCATTAGACTTTGAGAAAGCAGCAGACATGGATCTTGCAACTATGCTTCCCA 252

QY      41  AlaHisLysCysIleCysTyrPheProCys 50
      253  GCTCACAGTGTATCTGCTACTTTCCTTGT 282

RESULT 11
AR130280
LOCUS       AR130280
DEFINITION Sequence 58 from patent US 5538525.
ACCESSION  AR130280
VERSION     AR130280.1  GI:1603606
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unassigned.
REFERENCE    1 (bases 1 to 288)
AUTHORS      Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
              Terras,F.R.G. and Vanderleyden,J.
TITLE        Biocidal proteins
JOURNAL      Patent: US 5538525-A 58 23-JUL-1996;
              Location/Qualifiers
              source     1..288
              /organism="unassigned DNA"
              /mol_type="unassigned DNA"

ORIGIN

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Alignment Scores:
Pred. No.: 2,47e-27 Length: 288
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservative: 2
Best Local Similarity: 92.00% Mismatches: 2
Query Match: 93.36% Indels: 0
DB: 6 Gaps: 0

US-10-006-252A-10 (1-50) x I23736 (1-288)
QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 133 AAGTTGTGCCAAGGCCAAGTGGACATGTCAGGAGTCTGGAAACATTAACCATGC 192
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 193 AAGAATCAGTGCATTAGACTTGAAGAACACGACATGGATCTTGCACACTATGCTTCCCA 252
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 253 GCTCACAAGTGTATCTGCTACTTTCCTTGT 282

RESULT 12
AR014682
LOCUS AR014682 308 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 5 from patent US 5773696.
ACCESSION AR014682
VERSION AR014682.1 GI:3972136
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 308)
AUTHORS Liang,J., Shah,D.M., Wu,Y.Shun. and Rosenberger,C.Annette.
TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 5773696-A 5 30-JUN-1998;
FEATURES
source
Location/Qualifiers
/mol_type="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2,66e-27 Length: 308
Score: 281.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 93.36% Indels: 0
DB: 6 Gaps: 0

US-10-006-252A-10 (1-50) x AR014682 (1-308)
QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGGAGAGTCCAAAGTGGACATGTCAGGCGTGTGGAAACAAATGCTTGC 218
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 219 AAGATCAGTGCATTACCTTGAAGAGCNCGACATGATCTTGCAACTATGCTTCCCA 278

RESULT 13
AR432382
LOCUS AR432382 308 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6653280.
ACCESSION AR432382
VERSION AR432382.1 GI:40194659
KEYWORDS
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SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 308)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide AlyAPP from Alyssum and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 5 25-NOV-2003;
FEATURES
source
Location/Qualifiers
/mol_type="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2,66e-27 Length: 308
Score: 281.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 93.36% Indels: 0
DB: 6 Gaps: 0

US-10-006-252A-10 (1-50) x AR432382 (1-308)
QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGGAGAGTCCAAAGTGGACATGTCAGGCGTGTGGAAACAAATGCTTGC 218
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 219 AAGATCAGTGCATTACCTTGAAGAGCNCGACATGATCTTGCAACTATGCTTCCCA 278

RESULT 14
E34290
LOCUS E34290 449 bp DNA linear PAT 31-JAN-2002
DEFINITION Phase and plasmid constructed by ligating antibacterial protein gene DNA with vector DNA, transformant microorganism and transformant plant containing the same and antibacterial protein.
ACCESSION E34290
VERSION E34290.1 GI:18624295
KEYWORDS JP 2000116379-A/1.
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 449)
AUTHORS Shoji,K.
TITLE Phase and plasmid constructed by ligating antibacterial protein gene DNA with vector DNA, transformant microorganism and transformant plant containing the same and antibacterial protein
JOURNAL Patent: JP 2000116379-A 1 25-APR-2000;
COMMENT
OS Raphanus sativus L.
PN JP 2000116379-A/1
PD 25-APR-2000
PF 09-OCT-1998 JP 1998288472
PR
PI KAZUAKI SHOJI
PC C12N15/09,A01H5/00,A01N65/00,C07K14/415,C12N1/21,C12N5/10// PC (C12N15/09,C12R1:91),(C12N1/21,C12R1:19),(C12N5/10,C12R1:91), PC C12N15/00,
PC C12N5/00,(C12N15/00,C12R1:91),(C12N5/00,C12R1:91) CC
FH Key Location/Qualifiers
FT source 1..449
FT /organism='Raphanus sativus L.'
FT Location/Qualifiers
1..449
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
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ORIGIN

Alignment Scores: 4.04e-27 Length: 449
 Pred. No.: 281.00 Matches: 46
 Score: 281.00
 Percent Similarity: 96.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 6 Gaps: 0

US-10-006-252A-10 (1-50) x E34290 (1-449)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 131 AAGTTGGTCAGAGGCCAAGTGGACATGCTCAGGAGTCTGTGGAAATATTAACGATGC 190
 Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 191 AAGAATCAGTGCATTCGACTTGAGAAAGCACGACATGGGTCTTGGCAACTATGCTTCCCA 250

Qy 41 AlaHisIysCysIleCysTyrPheProCys 50

Db 251 GCTCAAGTGTATCTGTTATTCCCTTGT 280

RESULT 15

RSU18556 457 bp mRNA linear PLN 07-JUL-1995
 LOCUS Raphanus sativus antifungal protein 2 preprotein (Rs-AFP2) mRNA,
 DEFINITION complete cds.

ACCESSION U18556

VERSION U18556.1 GI:609319

KEYWORDS

SOURCE Raphanus sativus (radish)

ORGANISM

Raphanus sativus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.

REFERENCE

AUTHORS

Terras, F.R.G., Eggermont, K., Kovaleva, V., Raikhel, N.V.,
 Osborn, R.W., Kester, A., Rees, S.B., Torrekens, S., Van Leuven, F.,
 Vanderleyden, J., Cammue, B.P.A. and Broekaert, W.F.

TITLE

Small cysteine-rich antifungal proteins from radish: their role in
 host defense

JOURNAL

Plant Cell 7, 568-573 (1995)

REFERENCE

2 (bases 1 to 457)

AUTHORS

Terras, F.R.

TITLE

Direct Submission

JOURNAL

Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
 of Genetics, Applied Biological Sciences, W. De Croylaan 42,
 Heverlee, Belgium, B-3001

FEATURES

Location/Qualifiers

1..457

/organism="Raphanus sativus"

/mol_type="mRNA"

/strain="Ronde rode kleine witpunt"

/db_xref="taxon:3726"

/tissue type="seed"

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/gene="Rs-AFP2"

42..284

/gene="Rs-AFP2"

/function="antifungal, fungistatic"

/codon_start=1

/evidence=experimental

/product="antifungal protein 2 preprotein"

/protein_id="AAA69540.1"

/db_xref="GI:609320"

/translation="MAKFSASIVLLFVALVFAAPEPTWVEAKLCQRPSTWSGVC
 GNNWACKQKQIRLEKARHGSCNYPFAHKICVYPPC"

42..128

/sig_peptide

129..281

/gene="Rs-AFP2"

/mat_peptide

/gene="Rs-AFP2"

/product="antifungal protein 2"

/function="antifungal, fungistatic"

/note="Evidence for antifungal activity: Analysis of two
 novel classes of antifungal proteins from radish (Raphanus
 sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
 Chem. 267, 15301-15309"

/citation=[1]

/evidence=experimental

ORIGIN

Alignment Scores: 4.12e-27 Length: 457
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 Score: 281.00
 Percent Similarity: 96.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 8 Gaps: 0

US-10-006-252A-10 (1-50) x RSU18556 (1-457)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 132 AAGTTGGTCAGAGGCCAAGTGGACATGCTCAGGAGTCTGTGGAAATATTAACGATGC 191

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 192 AAGAATCAGTGCATTCGACTTGAGAAAGCACGACATGGGTCTTGGCAACTATGCTTCCCA 251

Qy 41 AlaHisIysCysIleCysTyrPheProCys 50

Db 252 GCTCAAGTGTATCTGTTATTCCCTTGT 281

Search completed: May 13, 2004, 11:35:46

Job time : 1735 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

QM protein - nucleic search, using frame_plus_p2n model

Run on: May 13, 2004, 09:41:12 ; Search time 349 Seconds
(without alignments)
608.624 Million cell updates/sec

Title: US-10-006-252A-10
Perfect score: 301
Sequence: 1 KLCERSGTSVGVCGNNAC.....QHSCNYYVPAKICVFPFC 50

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 337863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -LOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFM=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGEBUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: Geneseq2001bs.*
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7: Geneseq2003as.*
8: Geneseq2003bs.*
9: Geneseq2003cs.*
10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	281	93.4	261	2	AAQ38652
2	281	93.4	288	2	AAQ70130
3	281	93.4	308	2	AAQ70130 Antimicro
4	281	93.4	449	3	AAQ70130 Cloned 5'
5	281	93.4	522	3	AAQ70130 Raphanus
6	281	93.4	534	3	AAQ70130 DNA encod
7	281	93.4	534	3	AAQ70130 Portion o
8	281	93.4	534	3	AAQ70130 DNA encod
9	281	93.4	534	3	AAQ70130 DNA encod
10	281	93.4	534	3	AAQ70130 DNA encod

9	281	93.4	606	3	AAQ70130 DNA encod
10	279	92.7	243	3	AAQ70130 DNA encod
11	279	92.7	394	6	AAQ70130 DNA encod
12	279	92.7	414	2	AAQ70130 DNA encod
13	279	92.7	414	2	AAQ70130 DNA encod
14	279	92.7	414	2	AAQ70130 DNA encod
15	279	92.7	414	2	AAQ70130 DNA encod
16	279	92.7	414	2	AAQ70130 DNA encod
17	279	92.7	414	2	AAQ70130 DNA encod
18	274	91.0	243	6	AAQ70130 DNA encod
19	274	91.0	243	7	AAQ70130 DNA encod
20	274	91.0	403	2	AAQ70130 DNA encod
21	274	91.0	416	3	AAQ70130 DNA encod
22	272	90.4	243	6	AAQ70130 DNA encod
23	272	90.4	243	7	AAQ70130 DNA encod
24	272	90.4	400	2	AAQ70130 DNA encod
25	272	90.4	1616	2	AAQ70130 DNA encod
26	270	89.7	485	3	AAQ70130 DNA encod
27	267	88.7	270	2	AAQ70130 DNA encod
28	267	88.7	286	2	AAQ70130 DNA encod
29	267	88.7	481	2	AAQ70130 DNA encod
30	266	88.4	434	3	AAQ70130 DNA encod
31	266	88.4	437	3	AAQ70130 DNA encod
32	266	88.4	443	3	AAQ70130 DNA encod
33	266	88.4	446	3	AAQ70130 DNA encod
34	266	88.4	485	3	AAQ70130 DNA encod
35	266	88.4	485	3	AAQ70130 DNA encod
36	266	88.4	488	3	AAQ70130 DNA encod
37	266	88.4	557	3	AAQ70130 DNA encod
38	266	88.4	575	3	AAQ70130 DNA encod
39	266	88.4	1093	3	AAQ70130 DNA encod
40	264	87.7	500	2	AAQ70130 DNA encod
41	228	75.7	1973	3	AAQ70130 DNA encod
42	208	69.1	284	2	AAQ70130 DNA encod
43	208	69.1	284	2	AAQ70130 DNA encod
44	207	68.8	306	2	AAQ70130 DNA encod
45	162	53.8	150	2	AAQ70130 DNA encod

ALIGNMENTS

RESULT 1
AAQ38652
ID AAQ38652 standard; DNA; 261 BP.

XX AC AAQ38652;
XX AC AAQ38652;
DT 25-MAR-2003 (revised)
DT 07-JUL-1993 (first entry)
XX XX
DE RS-AFP2 cDNA.
XX XX
KW Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
KW fungicide; bactericide; antibiotic; antifungal; gram positive;
KW plant disease resistance; low toxicity.

OS Raphanus sativus.

XX Key Location/Qualifiers
FT CDS 16..256
FT FT /*tag= a

XX PN WO9305153-A1.

XX PD 18-MAR-1993.

XX PF 27-AUG-1992; 92WO-GB001570.

XX PR 29-AUG-1991; 91GB-00018523.

XX PR 13-FEB-1992; 92GB-00003038.

XX PR 25-JUN-1992; 92GB-00013526.

XX PA (ICIL) IMPERIAL CHEM IND PLC.

XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
 PI Vanderleyden J;
 XX WPI; 1993-100978/12.
 XX
 XX Biocidal proteins isolated from seeds of plants - e.g. brassica or
 PT dhania, useful for increasing plants' resistance to fungal and bacterial
 PT diseases.
 XX
 XX Example 21; Fig 35; 110pp; English.
 XX
 XX This cDNA represents the sequence of Rs-APP2 from *Raphanus sativus*. PCR
 CC primer AAQ38640 was used together with AAQ38641 to generate a probe for
 CC screening a *Raphanus sativus* seed cDNA library. This primer corresponds
 CC to amino acids 2 to 7 of Rs-APP1 and has a sense orientation. The 144bp
 CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a
 CC 123bp product, which was further reamplified with the same primers and
 CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
 CC product. This was used to screen a lambda ZAP11 cDNA library by in situ
 CC plaque hybridisation. Positive plaques were purified and subjected to two
 CC additional screening rounds with the same probe. Inserts were excised in
 CC vivo into the pBluescript phagemid form with the aid of helper phage
 CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and
 CC their size compared by agarose gel electrophoresis. Four clones had
 CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
 CC of the 4 largest clones were then sequenced and found to differ only in
 CC the length of their 5' and 3' UTR's. The longest sequence was identified
 CC as Rs-APP1 (AAQ38650). Rs-APP2 was seen to differ by only 2 amino acids
 CC from Rs-APP1, so the Rs-APP1 cDNA was transformed to the Rs-APP2
 CC nucleotide sequence by PCR assisted site directed mutagenesis. (Updated
 CC on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3,51e-26 Length: 261
 Score: 281.00 Matches: 46
 Percent Similarity: 96.00% Conservativeness: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 2 Gaps: 0
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 QY 1 LysLeuCysGluArgSerSerGlyThrTpsSerGlyValCysGlyAsnAsnAlaCys 20
 Db 106 AAGTTGTCGCAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGC 165
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 166 AAGAATCATGTCATTAGACTTGAAGAAGCACGACATGATCTTGCAACTATGTCTTCCCA 225
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 226 GCTCACAGTGTATCTGCTACTTCTTGT 255
 RESULT 2
 AAQ70130
 ID AAQ70130 standard; cDNA; 288 BP.
 AC
 XX AAQ70130;
 XX
 XX 25-MAR-2003 (revised)
 DT 14-FEB-1995 (first entry)
 XX
 XX Antimicrobial Rs-APP2.
 DE
 XX Antimicrobial; Rs-APP2; symbiosis; disease-resistance; fungus-resistance;
 KW Clavibacter xyli subsp. cynodentis; Cxc; crop improvement; endophyte;
 KW PCR; polymerase chain reaction; mutagenesis; ss.
 XX
 OS *Raphanus sativus*.

XX WO9416076-A1.
 PN 21-JUL-1994.
 XX
 XX 05-JAN-1994; 94WO-GB0000012.
 PF
 XX 08-JAN-1993; 93GB-00000281.
 PR
 XX (ZENE) ZENECA LTD.
 PA
 XX Dubock AC, Powell KA, Rees SB;
 PI WPI; 1994-249223/30.
 XX P-PSDB; AAR57327.
 DR
 XX Antimicrobial protein producing endo-symbiotic microorganisms - is
 PT produced by combining nucleic acids encoding the protein with an
 PT endophyte, useful for protecting plant hosts from esp. fungal disease.
 PT
 XX Disclosure; Page 33; 39pp; English.
 XX
 XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
 CC Clavibacter xyli subsp. cynodentis (Cxc). Plants or seeds treated with
 CC recombinant Cxc are protected against fungal disease. A suitable
 CC antimicrobial protein is Rs-APP1 from *R. sativus*. The full-length cDNA
 CC sequence of PCR assisted site-directed mutagenesis of Rs-APP2 is given in
 CC AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX
 SQ Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3,98e-26 Length: 288
 Score: 281.00 Matches: 46
 Percent Similarity: 96.00% Conservativeness: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 2 Gaps: 0
 US-10-006-252A-10 (1-50) x AAQ70130 (1-288)
 QY 1 LysLeuCysGluArgSerSerGlyThrTpsSerGlyValCysGlyAsnAsnAlaCys 20
 Db 133 AAGTTGTCGCAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACAATAACGCATGC 192
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 193 AAGAATCATGTCATTAGACTTGAAGAAGCACGACATGATCTTGCAACTATGTCTTCCCA 252
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 253 GCTCACAGTGTATCTGCTACTTCTTGT 282
 RESULT 3
 AAT94577
 ID AAT94577 standard; DNA; 308 BP.
 AC
 XX AAT94577;
 XX
 XX 12-MAY-1998 (first entry)
 DT
 XX Cloned 5' region of antifungal polypeptide cDNA.
 DE
 XX Antifungal polypeptide; AlyAPP; inhibition; transgenic plants;
 KW phytopathogenic fungus; resistance; ss.
 KW
 XX *Alyssum* sp.
 OS
 XX WO9737024-A2.
 PN
 XX 09-OCT-1997.
 PD
 XX

PF 27-MAR-1997; 97WO-US005709.
 XX
 PR 29-MAR-1996; 96US-00627706.
 XX
 PA (MONS) MONGANTO CO.
 XX
 XX Liang J, Shah D, Wu Y, Rosenberger CA;
 XX WPI; 1997-503109/46.
 XX
 DR Alyssum antifungal polypeptide and corresponding DNA - used in the
 XX production of transgenic plants resistant to phytopathogenic fungi.
 XX
 PT Example 4; Page 65; 92pp; English.
 XX
 CC This sequence is the product of the amplification of the 5' region of the
 CC antifungal polypeptide AlyAFP, isolated from plants of the Genus Alyssum,
 CC by a 5' RACE (Rapid Amplification of cDNA Ends) using primers AAT94575-
 CC T94576). The AlyAFP polypeptide can be used to control phytopathogenic
 CC fungi, whilst the coding DNA can be used to produce transgenic plants
 CC that express the polypeptide making them resistant to the phytopathogenic
 CC fungi
 XX
 SQ Sequence 308 BP; 78 A; 71 C; 78 G; 79 T; 0 U; 2 Other;
 Alignment Scores: Length: 308
 Pred. No.: 4,34e-26 Matches: 46
 Score: 281.00
 Percent Similarity: 94.00% Conservative: 1
 Best Local Similarity: 92.00% Mismatches: 3
 Query Match: 93.36% Indels: 0
 DB: 2 Gaps: 0
 US-10-006-252A-10 (1-50) x AAT94577 (1-308)
 QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 159 AAGTTGTGCGAGAGTCCCAAGTGAACATGTCAGGCGTGTGTGGAACACAAATGCTGC 218
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 219 AAGATCATGTCATTAACCTTGAAGGAGCGACATGATCTTGCACATATGCTCTCCCA 278
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 279 GCTCACAAGTGCATATGCTACTTCCCTGT 308
 RESULT 4
 AAA53190
 ID AAA53190 standard; DNA; 449 BP.
 AC AAA53190;
 XX
 DT 06-OCT-2000 (first entry)
 DE
 DE Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.
 KW Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;
 KW pathogenic microbe; radish; rice blast disease; ds.
 OS Raphanus sativus.
 XX
 XX JP2000116379-A.
 XX
 XX 25-APR-2000.
 XX
 XX 09-OCT-1998; 98JP-00288472.
 XX
 XX 09-OCT-1998; 98JP-00288472.
 XX
 XX (TOYA-) TOYAMA KEN.
 XX
 XX WPI; 2000-389821/34.
 DR

DR P-PSDB; AAY91117.
 XX
 PT Isolated DNA from Raphanus sativus used to transform a microbe and a
 PT plant to produce an antibacterial protein used to increase resistance of
 PT rice paddy against pathogenic microbes.
 XX
 XX Claim 1; Page 4; 7pp; Japanese.
 XX
 CC The present sequence encodes an antibacterial protein, designated
 CC radishin, isolated from Raphanus sativus (radish). A phase or plasmid
 CC comprising radishin can be used for increasing resistance of paddy and
 CC rice blast disease against pathogenic microbes
 XX
 SQ Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;
 Alignment Scores: Length: 449
 Pred. No.: 7,02e-26 Matches: 45
 Score: 281.00
 Percent Similarity: 96.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 3 Gaps: 0
 US-10-006-252A-10 (1-50) x AAA53190 (1-449)
 QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 131 AAGTTGTGTCAGAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAATATAACGATGC 190
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 191 AAGATCATGTCATTCGACTTGAGAAAGCGACATGGTCTTGCACATATGCTCTCCCA 250
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 251 GCTCACAAGTGCATCTGTTATTCCTTGT 280
 RESULT 5
 AAZ99324
 ID AAZ99324 standard; DNA; 522 BP.
 AC AAZ99324;
 XX
 DT 03-JUL-2000 (first entry)
 DE
 DE DNA encoding a fusion protein of DnaMpi and RsAPP2.
 KW Antimicrobial protein; AMPI; transgenic plant; linker peptide;
 KW protein expression; plant defensin; RsAPP2; antifungal protein; AFP2; ss.
 XX
 OS Synthetic.
 OS Dahlia merckii.
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FT misc_feature 160..309
 FT /tag= a
 FT /note= "encodes DnaMpi"
 FT misc_feature 358..510
 FT /tag= b
 FT /note= "encodes RsAPP2"
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 XX WO200011175-AI.
 XX
 XX 02-MAR-2000.
 XX
 XX 17-AUG-1999; 99WO-GB002716.
 XX
 XX 18-AUG-1998; 98GB-00018001.
 XX
 XX 04-DEC-1998; 98GB-00026753.
 XX
 XX (ZENE) ZENECA LTD.
 XX

PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
 XX WPI; 2000-246564/21.
 DR P-PSDB; AAY84057.
 XX
 PT Improving expression of polyproteins in plants involves coexpression of
 two or more proteins in plants within a single transcription unit.
 XX
 PS Example 2; Fig 8; 151pp; English.
 XX
 CC The present sequence encodes a protein of the invention, comprising the
 mature proteins of the plant defensins, the Dahlia antimicrobial protein
 (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker
 propeptide of the invention. The specification describes methods for
 improving expression levels of one or more proteins in a transgenic
 plant. The method comprises inserting a DNA sequence having a promoter
 region operably linked to two or more protein encoding regions separated
 by a DNA sequence coding for a linker propeptide and a terminator region.
 CC The method is used to produce proteins in plants. The linker propeptide
 comprising a cleavage site, whereby the expressed polypeptide is post-
 translationally processed into the component protein molecules. The
 CC propeptide sequence is rich in amino acids A, V, S and T and contains
 CC dipeptidic sequences consisting of either two acidic, two basic or one
 CC acidic and one basic residue as a cleavable linker sequence
 XX
 SQ Sequence 522 BP; 147 A; 119 C; 127 G; 129 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.51e-26 Length: 522
 Score: 281.00 Matches: 46
 Percent Similarity: 96.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 3 Gaps: 0
 US-10-006-252A-10 (1-50) x AAZ99324 (1-522)
 QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyValAsnAsnAlaCys 20
 DB 361 AAGTTGTCGAAGGCAAGTGGACATGTCTGAGTCTGTGGAAACAAATACGCATGC 420
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 DB 421 AAGAAATCAGTGCATTAGACTTGAGAAAGCAGACATGGATCTTGGCACTATGCTTCCCA 480
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 DB 481 GCTCACAAGTGTACTGCTACTTCTTCTGT 510
 RESULT 6
 AAZ51396
 ID AAZ51396 standard; DNA; 534 BP.
 AC AAZ51396;
 XX
 DT 06-JUN-2000 (first entry)
 XX
 DE Portion of pFAJ3106 encoding Dahlia merckii antimicrobial protein.
 KW Antimicrobial protein; DmAMP; transgenic plant; microbial infection;
 KW bacteria; fungi; field crop; fruit; vegetable; canola; banana; sunflower;
 KW apple; plant transformation vector; ds.
 XX
 OS Dahlia merckii.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 76..525
 FT /*tag= a
 FT /product= "Antimicrobial protein"
 FT
 PN W0200011196-A1.
 XX

PD 02-MAR-2000.
 XX
 PF 17-AUG-1999; 99WO-GB002720.
 XX
 PR 18-AUG-1998; 98GB-00018003.
 XX
 PA (ZENNE) ZENECA LTD.
 XX
 PI Evans IJ, Ray JA;
 XX
 DR WPI; 2000-237658/20.
 DR P-PSDB; AAY70323.
 XX
 FT Polynucleotide sequences and expression products useful for producing
 transgenic plants that are resistant to microbial infections.
 XX
 XX Example 3; Fig 7; 77pp; English.
 CC The present sequence corresponds to the region between XhoI and SacI
 sites of plant transformation vector pFAJ3106, which encompass the coding
 region for Dahlia merckii antimicrobial protein, Dm-AMP1. The vector is
 useful in the production of transgenic plants which show improved
 CC resistance to infections by microorganisms such as bacteria and fungi.
 CC Transgenic plants include e.g. field crops, fruits and vegetables, such
 CC as canola, sunflower, tomato, apple, banana, pear and mango
 XX
 SQ Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.76e-26 Length: 534
 Score: 281.00 Matches: 46
 Percent Similarity: 96.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 3 Gaps: 0
 US-10-006-252A-10 (1-50) x AAZ51396 (1-534)
 QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyValAsnAsnAlaCys 20
 DB 373 AAGTTGTCGAAGGCAAGTGGACATGTCTGAGTCTGTGGAAACAAATACGCATGC 432
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 DB 433 AAGAAATCAGTGCATTAGACTTGAGAAAGCAGACATGGATCTTGGCACTATGCTTCCCA 492
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 DB 493 GCTCACAAGTGTACTGCTACTTCTTCTGT 522
 RESULT 7
 AAZ99327
 ID AAZ99327 standard; DNA; 534 BP.
 AC AAZ99327;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE DNA encoding a fusion protein of DmAMP1 and RsAFP2.
 KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
 KW protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.
 XX
 OS Synthetic.
 OS Dahlia merckii.
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT CDS 76..522
 FT /*tag= a
 FT misc_feature 162..309
 FT /*tag= b
 FT /note= "encodes DmAMP1"
 FT

```

FT misc_feature 372..519
FT FT /*tag= c
XX OS /note= "encodes RsAFP2"
XX PN WO200011175-A1.
XX PD 02-MAR-2000.
XX PF 17-AUG-1999; 99WO-G8002716.
XX PR 18-AUG-1998; 98GB-00018001.
XX PR 04-DEC-1998; 98GB-00026753.
XX PA (ZENE ) ZENECA LTD.
XX BR Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX WPI; 2000-246564/21.
XX P-PSDB; AAY84060.
XX PT Improving expression of polyproteins in plants involves coexpression of
XX FT two or more proteins in plants within a single transcription unit.
XX PS Example 2; Fig 12; 151pp; English.
XX CC The present sequence encodes a protein of the invention, comprising the
XX CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX CC (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker
XX CC propeptide of the invention. The specification describes methods for
XX CC improving expression levels of one or more proteins in a transgenic
XX CC plant. The method comprises inserting a DNA sequence having a promoter
XX CC region operably linked to two or more protein encoding regions separated
XX CC by a DNA sequence coding for a linker propeptide and a terminator region.
XX CC The method is used to produce proteins in plants. The linker propeptide
XX CC comprising a cleavage site, whereby the expressed polypeptide is post-
XX CC translationally processed into the component protein molecules. The
XX CC propeptide sequence is rich in amino acids A, V, S and T and contains
XX CC dipeptidic sequences consisting of either two acidic, two basic or one
XX CC acidic and one basic residue as a cleavable linker sequence
XX SQ Sequence 534 BP; 154 A; 120 C; 125 G; 135 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.76e-26 Length: 534
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservativeness: 2
Best Local Similarity: 92.00% Mismatches: 0
Query Match: 93.36% Indels: 0
DB: 3 Gaps: 0

US-10-006-252A-10 (1-50) x AAZ99327 (1-534)
QY 1 LysLeuGlnCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 373 AAGTTGTGCCAAAGCCCAAGTGGACATGTCAGGAGTCGTGGAACCAATACCGATGC 432

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
DB 433 AAGATCATGTCGATAGACTTGAAGAACGACGACATGATCTTGCACTATGTCCTCCCA 492

QY 41 AlahisLysCysIleCysTyrPheProCys 50
DB 493 GCTCACAGTGTATCTGCTACTTTCCTTGT 522

RESULT 8
AAZ99325
ID AAZ99325 standard; DNA; 534 BP.
XX AC AAZ99325;
XX 03-JUL-2000 (first entry)
XX DT
XX DE DNA encoding a fusion protein of DmAMP1 and RsAFP2.

```

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XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
XX KW protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.
XX OS Synthetic.
XX OS Dahlia merckii.
XX OS Unidentified.
XX Key Location/Qualifiers
XX CDS 76..522
XX FT /*tag= a
XX FT 160..309
XX FT misc_feature /*tag= b
XX FT /note= "encodes DmAMP1"
XX FT 370..538
XX FT misc_feature /*tag= c
XX FT /note= "encodes RsAFP2"
XX PN WO200011175-A1.
XX PD 02-MAR-2000.
XX PF 17-AUG-1999; 99WO-G8002716.
XX PR 18-AUG-1998; 98GB-00018001.
XX PR 04-DEC-1998; 98GB-00026753.
XX PA (ZENE ) ZENECA LTD.
XX BR Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX WPI; 2000-246564/21.
XX P-PSDB; AAY84058.
XX PT Improving expression of polyproteins in plants involves coexpression of
XX FT two or more proteins in plants within a single transcription unit.
XX PS Example 2; Fig 9; 151pp; English.
XX CC The present sequence encodes a protein of the invention, comprising the
XX CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX CC (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker
XX CC propeptide of the invention. The specification describes methods for
XX CC improving expression levels of one or more proteins in a transgenic
XX CC plant. The method comprises inserting a DNA sequence having a promoter
XX CC region operably linked to two or more protein encoding regions separated
XX CC by a DNA sequence coding for a linker propeptide and a terminator region.
XX CC The method is used to produce proteins in plants. The linker propeptide
XX CC comprising a cleavage site, whereby the expressed polypeptide is post-
XX CC translationally processed into the component protein molecules. The
XX CC propeptide sequence is rich in amino acids A, V, S and T and contains
XX CC dipeptidic sequences consisting of either two acidic, two basic or one
XX CC acidic and one basic residue as a cleavable linker sequence
XX SQ Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.76e-26 Length: 534
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservativeness: 2
Best Local Similarity: 92.00% Mismatches: 0
Query Match: 93.36% Indels: 0
DB: 3 Gaps: 0

US-10-006-252A-10 (1-50) x AAZ99325 (1-534)
QY 1 LysLeuGlnCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 373 AAGTTGTGCCAAAGCCCAAGTGGACATGTCAGGAGTCGTGGAACCAATACCGATGC 432

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
DB 433 AAGATCATGTCGATAGACTTGAAGAACGACGACATGATCTTGCACTATGTCCTCCCA 492

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QY 41 AlahisLysCysileCysTyrPheProCys 50
 ID 493 GCTCACAGTGTATCTGCTACTTCTTCTGT 522
 Db

RESULT 9
 AAZ99326
 ID AAZ99326 standard; DNA; 606 BP.
 AC AAZ99326;
 XX

DT 03-JUL-2000 (first entry)
 XX
 DE DNA encoding a fusion protein of DnAMP1 and RsAFP2.
 KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
 KW protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.
 XX Synthetic.
 OS Dahlia merckii.
 OS Unidentified.

PH Key Location/Qualifiers
 FT CDS 76..597
 FT /*tag= a
 FT misc_feature 160..309
 FT /*tag= b
 FT /*note= "encodes DnAMP1"
 FT misc_feature 442..594
 FT /*tag= c
 FT /*note= "encodes RsAFP2"
 FT

WO200011175-A1.

XX 02-MAR-2000.
 XX 17-AUG-1999; 99WO-GB002716.
 XX 18-AUG-1998; 98GB-00018001.
 PR 04-DEC-1998; 98GB-00026753.
 XX (ZENE) ZENECA LTD.

PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
 XX WPI; 2000-246564/21.
 DR P-PSDB; AAY84059.

PT Improving expression of polyproteins in plants involves coexpression of
 PT two or more proteins in plants within a single transcription unit.

FS Example 2; Fig 11; 151pp; English.

CC The present sequence encodes a protein of the invention, comprising the
 CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
 CC (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker
 CC propeptide of the invention. The specification describes methods for
 CC improving expression levels of one or more proteins in a transgenic
 CC plant. The method comprises inserting a DNA sequence having a promoter
 CC region operably linked to two or more protein encoding regions separated
 CC by a DNA sequence coding for a linker propeptide and a terminator region.
 CC The method is used to produce proteins in plants. The linker propeptide
 CC comprising a cleavage site, whereby the expressed polypeptide is post-
 CC translationally processed into the component protein molecules. The
 CC propeptide sequence is rich in amino acids A, V, S and T and contains
 CC dipeptidic sequences consisting of either two acidic, two basic or one
 CC acidic and one basic residue as a cleavable linker sequence

SQ Sequence 606 BP; 189 A; 136 C; 137 G; 144 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.03e-25 Length: 606
 Score: 281.00 Matches: 46

Percent Similarity: 96.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 3 Gaps: 0

US-10-006-252A-10 (1-50) x AAZ99326 (1-606)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyValCysGlyValCys 20
 ID 445 AAGTTGTGCCAAAGGCGAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGC 504
 Db
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 ID 505 AAGATCAGTCATAGACTTGGAGAAAGCAGACATGATGCACTTGCACATCTATGCTCTCCCA 564
 Db
 QY 41 AlahisLysCysileCysTyrPheProCys 50
 ID 565 GCTCACAGTGTATCTGCTACTTCTTCTGT 594
 Db

RESULT 10

ABQ82690
 ID ABQ82690 standard; cDNA; 243 BP.

XX AC ABQ82690;

XX DT 02-JAN-2003 (first entry)

XX DE Wasabia japonica gamma-thionin encoding cDNA SEQ ID NO:1.

XX KW Wasabia japonica; gamma-thionin; plant; disease-resistant plant; gene;
 XX SS.

XX OS Eutrema wasabi.

XX FH Key Location/Qualifiers

XX CDS 1..243
 FT /*tag= a
 FT /product= "gamma-thionin"

XX JP2002272292-A.

XX 24-SEP-2002.

XX 22-MAR-2001; 2001JP-00083526.

XX 22-MAR-2001; 2001JP-00083526.

XX (IWAT-) IWATE KEN.

XX WPI; 2002-718704/78.

XX P-PSDB; ABP53725.

XX A disease-resistant plant in which wasabi gamma-thionin gene is
 PT introduced, creation of the disease-resistant plant.

XX Claim 3; Page 8; 11pp; Japanese.

CC The present invention describes a disease-resistant plant in which a
 CC wasabi gamma-thionin gene is introduced. Also described is a method for
 CC the creation of the above disease-resistant plant by introducing a wasabi
 CC gamma-thionin gene to a plant. The present sequence encodes a Eutrema
 CC wasabi (Wasabia japonica) gamma-thionin protein from the present
 CC invention

SQ Sequence 243 BP; 60 A; 54 C; 55 G; 74 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 5.69e-26 Length: 243
 Score: 279.00 Matches: 44
 Percent Similarity: 96.00% Conservative: 4
 Best Local Similarity: 88.00% Mismatches: 2
 Query Match: 92.69% Indels: 0
 DB: 6 Gaps: 0

US-10-006-252A-10 (1-50) x ABQ82690 (1-243)		Best Local Similarity: 92.00%	Mismatches: 3
Query Match: 92.69%		Indels: 0	
DB: 9		Gaps: 0	
US-10-006-252A-10 (1-50) x ADC51221 (1-394)			
Qy	1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20		
Db	91 AAGTTGGCGAGAGTCAAGTGGACATGGTCAGGAGTCTGTGGAAACAACAATCGTGC 150		
Qy	21 LysAsnGlnCysLeuArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40		
Db	151 AAGAATCAGTGCATCAACCTTGAGGAGCAGCATGGATCTTGCAACTATATCTTCCCA 210		
Qy	41 AlaHisCysCysLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 50		
Db	211 TATCACAGATGATCTCTTACTTCCCATGT 240		
RESULT 11			
ID	ADC51221 standard; DNA; 394 BP.		
AC	ADC51221;		
DT	18-DEC-2003 (first entry)		
DE	Brassica oleracea defensin protein coding sequence.		
KW	antimicrobial protein; defensin; transgenic plant;		
KW	composite disease resistance; pathogenic bacteria;		
KW	rice white leaf blight; brown-stripe disease; glume blight;		
KW	seedling damping-off disease; filamentous fungi; rice blight;		
KW	sheath blight disease; leaf blight; gene; ds.		
OS	Brassica oleracea.		
Key	Location/Qualifiers		
FT	1..243		
FT	/*tag= a		
FT	/product= "Brassica oleracea defensin protein"		
XX			
PN	JP2003088379-A.		
XX			
PD	25-MAR-2003.		
PF	18-SEP-2001; 2001JP-00283117.		
PR	18-SEP-2001; 2001JP-00283117.		
PA	(DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.		
XX			
DR	WPI; 2003-621123/59.		
DR	P-PSDB; ADC51222.		
XX			
PT	Novel protein from Brassica campestris, useful as antimicrobial against		
PT	plant pathogenic filamentous fungi or pathogenic bacteria, especially for		
PT	treating e.g. rice white leaf blight and sheath blight disease.		
XX			
PS	Claim 3; SEQ ID NO 1; 34pp; Japanese.		
XX			
CC	The invention comprises the amino acid and coding sequences of		
CC	antimicrobial (defensin) proteins from Brassica. The DNA and protein		
CC	sequences of the invention are useful for producing transformed plants		
CC	with composite disease resistance, especially resistant to diseases		
CC	caused by pathogenic bacteria, such as: rice white leaf blight, brown-		
CC	stripe disease, glume blight, and seedling damping-off disease. As well		
CC	as diseases caused by filamentous fungi, such as: rice blight, sheath		
CC	blight disease, and leaf blight. The present DNA sequence encodes a		
CC	Brassica defensin protein of the invention.		
XX			
SQ	Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	1..06e-25	Length:	394
Score:	279.00	Matches:	46
Percent Similarity:	94.00%	Conservative:	1
US-10-006-252A-10 (1-50) x ADC51221 (1-394)			
Qy	1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20		
Db	91 AAGTTGGCGAGAGTCAAGTGGACATGGTCAGGAGTCTGTGGAAACAACAATCGTGC 150		
Qy	21 LysAsnGlnCysLeuArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40		
Db	151 AAGAATCAGTGCATCAACCTTGAGGAGCAGCATGGATCTTGCAACTATATCTTCCCA 210		
Qy	41 AlaHisCysCysLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 50		
Db	211 TATCACAGATGATCTCTTACTTCCCATGT 240		
RESULT 12			
ID	AAQ38650 standard; DNA; 414 BP.		
XX	AAQ38650;		
DT	25-MAR-2003 (revised)		
DT	07-JUL-1993 (first entry)		
DE	Rs-AFP1 cDNA.		
XX			
KW	Raphanus sativus; Brassica; Arabidopsis; Chnicus; Lathyrus; Clitoria;		
KW	fungicide; bactericide; antibiotic; antifungal; gram positive;		
KW	plant disease resistance; low toxicity.		
OS	Raphanus sativus.		
Key	Location/Qualifiers		
FT	16..256		
FT	/*tag= a		
XX			
PN	WO9305153-A1.		
XX			
PD	18-MAR-1993.		
PF	27-AUG-1992; 92WO-GB001570.		
XX			
PR	29-AUG-1991; 91GB-00018523.		
PR	13-FEB-1992; 92GB-00003038.		
PR	25-JUN-1992; 92GB-00013526.		
XX			
PA	(ICIL) IMPERIAL CHEM IND PLC.		
XX			
PI	Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras PRG;		
PI	Vanderleyden J;		
XX			
DR	WPI; 1993-100978/12.		
XX			
PT	Biocidal proteins isolated from seeds of plants - e.g. brassica or		
PT	dahlia, useful for increasing plants' resistance to fungal and bacterial		
PT	diseases.		
XX			
PS	Example 21; Fig 35; 110pp; English.		
XX			
CC	This cDNA represents the sequence of Rs-AFP1 from Raphanus sativus. PCR		
CC	primer AAQ38640 was used together with AAQ38641 to generate a probe for		
CC	screening a Raphanus sativus seed cDNA library. This primer corresponds		
CC	to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp		
CC	product was partially re-amplified using AAQ38642 and AAQ38641 to give a		
CC	123bp product, which was further reamplified with the same primers and		
CC	digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR		
CC	product. This was used to screen a lambda ZAPII cDNA library by in situ		
CC	plaque hybridisation. Positive plaques were purified and subjected to two		
CC	additional screening rounds with the same probe. Inserts were excised in		
CC	vivo into the paluescript phagemid form with the aid of helper phage		

CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and
CC their size compared by agarose gel electrophoresis. Four clones had
CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
CC of the 4 largest clones were then sequenced and found to differ only in
CC the length of their 5' and 3' UTR's. The longest sequence is given here.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 1.12e-25 Length: 414
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservativity: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 2 Gaps: 0

US-10-006-252A-10 (1-50) x AAQ38650 (1-414)

OY 1 LysLeuCySGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

DB 106 AAGTTGTCGAAAGCCCAAGTGGGACATGCTCAGGAGTCTGTGGAACAATAACGCATGC 165

OY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyValPhePro 40

DB 166 AAGAATCAGTGCATTAACTTGAGAAAGCAGCATGGATCTTGCAACTATGCTCTCCCA 225

OY 41 AlaHisLysCysIleCysTyPheProCys 50

DB 226 GCTCACAAGTGTACTCTCTTCTTGT 255

RESULT 13

AAQ70128

ID AAQ70128 standard; cDNA; 414 BP.

XX AC AAQ70128;

XX DT 25-MAR-2003 (revised)

XX DT 14-FEB-1995 (first entry)

XX DE Antimicrobial Rs-AFP1.

XX KW Antimicrobial; Rs-AFP1; symbiosis; disease-resistance; fungus-resistance;

XX KW Clavibacter xylis subsp. cynodontis; Cxc; crop improvement; endophyte; ss.

XX OS Raphanus sativus.

XX PN WO9416076-A1.

XX PD 21-JUL-1994.

XX PF 05-JAN-1994; 94WO-GB0000012.

XX PR 08-JAN-1993; 93GB-00000281.

XX PA (ZENE) ZENECA LTD.

XX PI Dubock AC, Powell KA, Rees SB;

XX XX WPI; 1994-249223/30.

XX DR P-PSDB; AAR57325.

XX XX Antimicrobial protein producing endo-symbiotic microorganisms - is

XX PT produced by combining nucleic acids encoding the protein with an

XX PT endophyte, useful for protecting plant hosts from esp. fungal disease.

XX XX Disclosure; Page 31; 39pp; English.

XX CC Plant-derived antimicrobial proteins are expressed in endosymbiotic

XX CC Clavibacter xylis subsp. cynodontis (Cxc). Plants or seeds treated with

XX CC recombinant Cxc are protected against fungal disease. A suitable

XX CC antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA

XX CC sequence of Rs-AFP1 is given in AAQ70128. (Updated on 25-MAR-2003 to

CC correct PN field.)

XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.12e-25 Length: 414
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservativity: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 2 Gaps: 0

US-10-006-252A-10 (1-50) x AAQ70128 (1-414)

OY 1 LysLeuCySGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

DB 106 AAGTTGTCGAAAGCCCAAGTGGGACATGCTCAGGAGTCTGTGGAACAATAACGCATGC 165

OY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyValPhePro 40

DB 166 AAGAATCAGTGCATTAACTTGAGAAAGCAGCATGGATCTTGCAACTATGCTCTCCCA 225

OY 41 AlaHisLysCysIleCysTyPheProCys 50

DB 226 GCTCACAAGTGTACTCTCTTCTTGT 255

RESULT 14

AAQ72333

ID AAQ72333 standard; cDNA; 414 BP.

XX AC AAQ72333;

XX DT 25-MAR-2003 (revised)

XX DT 19-JAN-1998 (first entry)

XX DE Raphanus sativus antifungal protein I (Rs-AFP1) cDNA.

XX KW Antifungal protein; candida; fungal resistance; food additive; radish;

XX KW crop protection; plant defensin; bacterial protection; preservative; ss.

XX OS Raphanus sativus.

XX PH Key Location/Qualifiers

XX FT CDS 16..258

XX FT /tag= a

XX FT /transl_except= (pos:85..87, aa:Glu)

XX FT sig_peptide 16..102

XX FT /tag= b

XX FT mat_peptide 103..255

XX FT /tag= c

XX FT /product= "antifungal_protein_1"

XX PN WO9721815-A2.

XX XX 19-JUN-1997.

XX PF 12-DEC-1996; 96WO-GB003068.

XX PR 13-DEC-1995; 95GB-00025455.

XX PR 28-MAR-1996; 96GB-00006552.

XX PA (ZENE) ZENECA LTD.

XX XX Meloen RH, Puijk WC, Schaaper WM, Sijtsma L, Van Amerongen A;

XX PI Broekaert W, Samblanx GW, Fart F, Borremans FAM, Rees SB;

XX PI Van Gelder WMJ;

XX XX WPI; 1997-332786/30.

XX DR P-PSDB; AAM19280.

XX PT Antifungal peptide derived from radish antifungal protein 2 - and related

XX PT DNA, useful for producing plants with increased fungal resistance and as

XX PT therapeutic or preservative agent.

XX PS Claim 8; Fig 2; 65pp; English.
 XX CC This cDNA sequence encodes an Raphanus sativus (radish) antifungal
 CC protein (Rs-APF1). Analogues of the homologous protein, Rs-APP2
 CC (AAW19281), have also been produced (see AAW19282-92, AAW19294-98,
 CC AAW19301-04, AAW19330-34 and AAW31765-834). Plants containing DNA
 CC sequences encoding these proteins have improved resistance to fungi.
 CC Compositions containing the peptides can be used to control fungi or
 CC bacteria in pharmaceutical (e.g. treatment of Candida infections) or
 CC preservative purposes (as food additives). In agriculture, the peptide
 CC may be used to improve disease resistance or disease tolerance of crops,
 CC either pre or post harvest. When applied to plants they may also have
 CC curative as well as protective actions. The peptides may also be used to
 CC protect plants by introducing them, or a microorganism capable of
 CC expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct
 CC PI field.)
 XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,12e-25 Length: 414
 Score: 279.00 Matches: 46
 Percent Similarity: 94.00% Conservative: 1
 Best Local Similarity: 92.00% Mismatches: 3
 Query Match: 92.69% Indels: 0
 DB: 2 Gaps: 0

US-10-006-252A-10 (1-50) x AAT72333 (1-414)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 106 AAGTTGTGCGAAAGCCAAAGTGGGACATGGTCAGAGTCTGTGGAACATAACGCATGC 165
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 166 AAGATCAGTGCATTAACTTGAGAACGACGACATGGATCTTGCACTATGCTTCCCA 225
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 226 GCTCACAGTGTATCTGCTACTTCTTGT 255

RESULT 15

ID AAT68696 standard; cDNA; 414 BP.

XX AC AAT68696;

XX DT 13-DEC-1997 (first entry)

XX DE Radish antifungal protein 1 (Rs-APF1) cDNA.

XX KW Rs-APF1; radish antifungal protein 1; fungicide; salt tolerance;
 XX KW preservative; transgenic plant; crop protection.

XX OS Raphanus sativus.

XX FH Key Location/Qualifiers

XX FT CDS 15..258

XX FT /tag= a

XX FT /transl_except= (pos:85..87, aa:Glu)

XX FT sig_peptide 16..102

XX FT /tag= b

XX FT mat_peptide 103..255

XX FT /tag= c

XX DN WO9721814-A1.

XX XX 19-JUN-1997.

XX XX 12-DEC-1996; 96WO-GB003065.

XX XX 13-DEC-1995; 95GB-00025474.

XX PA

(ZENE) ZENECA LTD.

XX PI Broekaert WF, De Samblaux GW, Rees SB;

XX DR WPI; 1997-332785/30.

XX DR P-PSDB; AAW19617.

PT New active mutants of radish antifungal protein 2 - used to generate
 fungus-resistant plants or as therapeutic or preservative agents.

PS Disclosure; Fig 2; 39pp; English.

XX CC This cDNA clone codes for the preprotein for radish antifungal protein 1
 CC (Rs-APF1) (AAW19617). Novel antifungal proteins are based on Rs-APF1, Rs-
 CC APP2 (see AAW19616), Rs-APP3 and Rs-APP4, especially those in which Gly9
 CC is replaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by
 CC Met. Mutants (see AAW26371-90) of Rs-APP2 are specifically claimed. The
 CC mutants show improved salt tolerant antifungal activity, particularly
 CC when expressed in plants

XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,12e-25 Length: 414
 Score: 279.00 Matches: 46
 Percent Similarity: 94.00% Conservative: 1
 Best Local Similarity: 92.00% Mismatches: 3
 Query Match: 92.69% Indels: 0
 DB: 2 Gaps: 0

US-10-006-252A-10 (1-50) x AAT68696 (1-414)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 106 AAGTTGTGCGAAAGCCAAAGTGGGACATGGTCAGAGTCTGTGGAACATAACGCATGC 165

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 166 AAGATCAGTGCATTAACTTGAGAACGACGACATGGATCTTGCACTATGCTTCCCA 225

QY 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 226 GCTCACAGTGTATCTGCTACTTCTTGT 255

Search completed: May 13, 2004, 11:06:38

Job time : 350 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 13, 2004, 10:54:53 ; Search time 85 Seconds
(without alignments)
326.442 Million cell updates/sec

Title: US-10-006-252A-10

Perfect score: 301

Sequence: 1 KLCERSSTGWSGCGNNAC.....QHGSNYPVPAHKICICYPC 50

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Issued Patents NA -QFMT=fastap -SUFFIX=arni -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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5: /cgn2_6/ptodata/2/ina/6C COMB.seq.*
6: /cgn2_6/ptodata/2/ina/6D COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	281	93.4	285	1	US-08-627-706-17
2	281	93.4	285	3	US-09-103-489-17
3	281	93.4	285	4	US-09-829-381D-17
4	281	93.4	288	1	US-08-377-687-58
5	281	93.4	288	3	US-08-971-982-58
6	281	93.4	288	3	US-08-971-982-58
7	281	93.4	308	1	US-08-627-706-5
8	281	93.4	308	3	US-09-103-489-5
9	281	93.4	308	4	US-09-829-381D-5
10	279	92.7	285	1	US-08-627-706-16
11	279	92.7	285	3	US-09-103-489-16
12	279	92.7	285	4	US-09-829-381D-16

13	279	92.7	414	1	US-08-377-687-48	Sequence 48, Appl
14	279	92.7	414	1	US-08-777-192-48	Sequence 48, Appl
15	279	92.7	414	3	US-08-971-982-48	Sequence 48, Appl
16	279	92.7	414	4	US-09-077-951-19	Sequence 19, Appl
17	279	92.7	414	4	US-09-077-948A-45	Sequence 45, Appl
18	267	88.7	270	1	US-08-627-706-14	Sequence 14, Appl
19	267	88.7	270	3	US-09-103-489-14	Sequence 14, Appl
20	267	88.7	270	3	US-09-829-381D-14	Sequence 14, Appl
21	267	88.7	286	1	US-08-627-706-12	Sequence 12, Appl
22	267	88.7	286	3	US-09-103-489-12	Sequence 12, Appl
23	267	88.7	286	4	US-09-829-381D-12	Sequence 12, Appl
24	264	87.7	500	1	US-08-627-706-9	Sequence 9, Appl
25	264	87.7	500	3	US-09-103-489-9	Sequence 9, Appl
26	264	87.7	500	4	US-09-829-381D-9	Sequence 9, Appl
27	208	69.1	284	1	US-08-377-687-50	Sequence 50, Appl
28	208	69.1	284	1	US-08-777-192-50	Sequence 50, Appl
29	208	69.1	284	3	US-08-971-982-50	Sequence 50, Appl
30	207	68.8	306	1	US-08-627-706-8	Sequence 8, Appl
31	207	68.8	306	3	US-09-103-489-8	Sequence 8, Appl
32	207	68.8	306	4	US-09-829-381D-8	Sequence 8, Appl
33	162	53.8	150	1	US-08-377-687-31	Sequence 31, Appl
34	162	53.8	150	1	US-08-777-192-31	Sequence 31, Appl
35	162	53.8	150	3	US-08-971-982-31	Sequence 31, Appl
36	159	52.8	150	1	US-08-377-687-34	Sequence 34, Appl
37	159	52.8	150	1	US-08-777-192-34	Sequence 34, Appl
38	159	52.8	150	3	US-08-971-982-34	Sequence 34, Appl
39	157	52.2	150	1	US-08-377-687-33	Sequence 33, Appl
40	157	52.2	150	1	US-08-777-192-33	Sequence 33, Appl
41	157	52.2	150	3	US-08-971-982-33	Sequence 33, Appl
42	154	51.2	565	4	US-09-589-733C-6	Sequence 6, Appl
43	141.5	47.0	147	1	US-08-377-687-36	Sequence 36, Appl
44	141.5	47.0	147	1	US-08-777-192-36	Sequence 36, Appl
45	141.5	47.0	147	3	US-08-971-982-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-627-706-17
; Sequence 17, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; CONTROLLING PLANT PATHOGENIC FUNGI
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 17:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-08-627-706-17
Alignment Scores:
Pred. No.: 3 12e-28 Length: 285
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservative: 2
Best Local Similarity: 92.00% Mismatches: 2
Query Match: 93.36% Indels: 0
DB: 1 Gaps: 0

US-10-006-252a-10 (1-50) x US-08-627-706-17 (1-285)
QY 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 121 AAGTTGTGCAAGGCGCATCGAGGACTTGGTCAGGAGTCTGGGAAACAAACACGCGATGC 180
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
DB 181 AAGAACCAATGCATCAGACTCGAAGAGCGACGGCATGATCTTGCAACTACGTCTTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
DB 241 GCTCACAGTGCATCTGCTACTTTCCATGC 270

RESULT 2
US-09-103-489-17
; Sequence 17, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 17
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-829-381D-17
Alignment Scores:
Pred. No.: 3 12e-28 Length: 285
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservative: 2
Best Local Similarity: 92.00% Mismatches: 2
Query Match: 93.36% Indels: 0
DB: 4 Gaps: 0

US-10-006-252a-10 (1-50) x US-09-829-381D-17 (1-285)
QY 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 121 AAGTTGTGCAAGGCGCATCGAGGACTTGGTCAGGAGTCTGGGAAACAAACACGCGATGC 180
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
DB 181 AAGAACCAATGCATCAGACTCGAAGAGCGACGGCATGATCTTGCAACTACGTCTTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
DB 241 GCTCACAGTGCATCTGCTACTTTCCATGC 270

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-08-627-706-17
Alignment Scores:
Pred. No.: 3 12e-28 Length: 285
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservative: 2
Best Local Similarity: 92.00% Mismatches: 2
Query Match: 93.36% Indels: 0
DB: 1 Gaps: 0

US-10-006-252a-10 (1-50) x US-08-627-706-17 (1-285)
QY 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 121 AAGTTGTGCAAGGCGCATCGAGGACTTGGTCAGGAGTCTGGGAAACAAACACGCGATGC 180
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
DB 181 AAGAACCAATGCATCAGACTCGAAGAGCGACGGCATGATCTTGCAACTACGTCTTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
DB 241 GCTCACAGTGCATCTGCTACTTTCCATGC 270

RESULT 2
US-09-103-489-17
; Sequence 17, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,489
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
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RESULT 4

US-08-377-687-58
 ; Sequence 58, Application US/08377687
 ; Patent No. 5538525
 ; GENERAL INFORMATION:
 ; APPLICANT: BROEKAERT, WILLEM F.
 ; APPLICANT: CAMMUE, BRUNO P.A.
 ; APPLICANT: OSBORN, RUPERT W.
 ; APPLICANT: REES, SARAH B.
 ; APPLICANT: TERRAS, FRANKY R.G.
 ; APPLICANT: VANDERLEVDEN, JOZEF
 ; TITLE OF INVENTION: BIOCIDAL PROTEINS
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 ; STREET: 1100 NEW YORK AVENUE, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/377,687
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/002,480
 ; FILING DATE: 04-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOKULIS, PAUL N.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-861-3000
 ; TELEFAX: 202-822-0944
 ; INFORMATION FOR SEQ ID NO: 58:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 288 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 43..282
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 US-08-377-687-58

Alignment Scores:
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 Query Match: 93.36% Indels: 0
 DB: 1 Gaps: 0

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RESULT 5

US-08-777-192-58
 ; Sequence 58, Application US/08777192
 ; Patent No. 5824869
 ; GENERAL INFORMATION:
 ; APPLICANT: BROEKAERT, WILLEM F.
 ; APPLICANT: CAMMUE, BRUNO P.A.
 ; APPLICANT: OSBORN, RUPERT W.
 ; APPLICANT: REES, SARAH B.
 ; APPLICANT: TERRAS, FRANKY R.G.
 ; APPLICANT: VANDERLEVDEN, JOZEF
 ; TITLE OF INVENTION: BIOCIDAL PROTEINS
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 ; STREET: 1100 NEW YORK AVENUE, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/777,192
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/002,480
 ; FILING DATE: 04-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOKULIS, PAUL N.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-861-3000
 ; TELEFAX: 202-822-0944
 ; INFORMATION FOR SEQ ID NO: 58:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 288 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 43..282
 ;
 US-08-777-192-58

Alignment Scores:
 Pred. No.: 3.17e-28 Length: 288
 Score: 281.00 Matches: 46
 Percent Similarity: 96.00% Conservative: 2
 Best Local Similarity: 92.00% Mismatches: 2
 Query Match: 93.36% Indels: 0
 DB: 1 Gaps: 0

US-10-006-252A-10 (1-50) x US-08-777-192-58 (1-288)

Qy	1	LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys	20
Db	133	AAAGTGTGCCAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAAACATAACCGATGC	192
Qy	21	LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro	40
Db	193	AAGAATCAGTGCATTAGACTTGAGAAAGCACGACATGATCTTGCACATATGCTCTCCCA	252
Qy	41	AlaHisLysCysIleCysTyrPheProCys	50
Db	253	GCTCACAGTGTATCTGCTACTTTCTTGT	282

RESULT 6

US-08-971-982-58
; Sequence 58, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKART, WILLEM F.
; CAMMUE, BRUNO P.A.
; OSBORN, RUPERT W.
; REES, SARAH B.
; TERRAS, FRANKY R.G.
; VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARRY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,982
; FILING DATE: 17-No. 6187904-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..282
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-08-971-982-58

Alignment Scores:
Pred. No.: 3.17e-28 Length: 288
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservative: 2
Best Local Similarity: 92.00% Mismatches: 2
Query Match: 93.36% Indels: 0
DB: 3 Gaps: 0
US-10-006-252A-10 (1-50) x US-08-971-982-58 (1-288)
QY 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 133 AAGTTGTCGAAGGCAAGTGGAGCATGTCAGGAGTCTGGGAACAATAACGATGC 192
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 193 AAGAATCAGTGCATTAGACTTTGAGAAAGCACGACATGATCTTGCAACTATGCTTCCCA 252
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 253 GCTCACAAGGTATCTGCTACTTTCCTTGT 282

RESULT 7

US-08-627-706-5
; Sequence 5, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, B84F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-627-706-5

Alignment Scores:
Pred. No.: 3.46e-28 Length: 308
Score: 281.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 93.36% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-10 (1-50) x US-08-627-706-5 (1-308)

QY 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTCGAGAGTCCCAAGTGGACATGTCAGCGTGTGTGGAACAACAATGCTTGC 218
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 219 AAGAATCAGTGCATTAACTTGAAGAGCAGCATGATCTTGCAACTATGCTTCCCA 278
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 279 GCTCACAAGTGCATTATGCTTTCCTTGT 308

RESULT 8

US-09-103-489-5
; Sequence 5, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong


```

; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,489
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-103-489-5

Alignment Scores:
Pred. No.: 3,46e-28 Length: 308
Score: 281.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 93.36% Indels: 0
DB: 3 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-103-489-5 (1-308)

QY 1 LysleuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGCCAGAGTCCAAAGTGGAAACATGCTCAGCGGTGTGTGGAACAACAATGCTTGC 218
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 219 AAGAATCAGTGCATTAACCTTGAAGGAGCNCACATGGATCTTGCACACTATGCTCTCCCA 278
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 279 GCTCACAGTGCATATGCTACTTCCCTGT 308

RESULT 9
US-09-829-381D-5
; Sequence 5, Application US/09829381D
; Patent No. 6653280
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyesum and Methods for Contro
; TITLE OF INVENTION: Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D

; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 5
; LENGTH: 308
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic PCR reaction product
; NAME/KEY: misc feature
; LOCATION: (22)..(248)
; OTHER INFORMATION: N = any nucleotide
US-09-829-381D-5

Alignment Scores:
Pred. No.: 3,46e-28 Length: 308
Score: 281.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 93.36% Indels: 0
DB: 4 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-829-381D-5 (1-308)

QY 1 LysleuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGCCAGAGTCCAAAGTGGAAACATGCTCAGCGGTGTGTGGAACAACAATGCTTGC 218
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 219 AAGAATCAGTGCATTAACCTTGAAGGAGCNCACATGGATCTTGCACACTATGCTCTCCCA 278
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 279 GCTCACAGTGCATATGCTACTTCCCTGT 308

RESULT 10
US-08-627-706-16
; Sequence 16, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
```

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; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-08-627-706-16

Alignment Scores:
Pred. No.: 5,69e-28 Length: 285
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-10 (1-50) x US-08-627-706-16 (1-285)
QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCGAGAGCCATCAGGGACTTGTTCAGAGTCTGCGGAAACAAACAGCATGC 180
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCAATGCATCAACTCGAGAGGACGGCATGATCTTGCAACTACGTCCTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCAAGTGCATCTGCTACTTTCCATGC 270

RESULT 11
US-09-103-489-16
; Sequence 16, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, B84F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,489
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-09-103-489-16

Alignment Scores:
Pred. No.: 5,69e-28 Length: 285
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 3 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-103-489-16 (1-285)
QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCGAGAGCCATCAGGGACTTGTTCAGAGTCTGCGGAAACAAACAGCATGC 180
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCAATGCATCAACTCGAGAGGACGGCATGATCTTGCAACTACGTCCTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCAAGTGCATCTGCTACTTTCCATGC 270

RESULT 12
US-09-829-381D-16
; Sequence 16, Application US/09829381D
; Patent No. 6653280
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
; TITLE OF INVENTION: Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 16
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-829-381D-16

Alignment Scores:
Pred. No.: 5,69e-28 Length: 285
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 4 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-829-381D-16 (1-285)
QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCGAGAGCCATCAGGGACTTGTTCAGAGTCTGCGGAAACAAACAGCATGC 180
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCAATGCATCAACTCGAGAGGACGGCATGATCTTGCAACTACGTCCTCCCA 240
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
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Db 241 GCTCACAGTGCATCTGCTACTTTCCATGC 270

RESULT 13

US-08-377-687-48
; Sequence 48, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKERT, WILLEM F.
; APPLICANT: CAMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARB & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 16..255
US-08-377-687-48

Alignment Scores:
Pred. No.: 9.24e-28 Length: 414
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-10 (1-50) x US-08-377-687-48 (1-414)

Qy 1 LysLeuCysGluArgSerSerglyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 106 AAGTTGTGCGAAAGGCCAAGTGGACATGCTCAGGAGTCTGTGGAACAATAACGCATGC 165

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 166 AAGAAATCAGTGCATTAACTTGAAGAACGACGATGGATCTTGGAACTATGCTCTCCCA 225

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 226 GCTCACAGTGTACTCTACTTCTTCTGT 255

RESULT 14

US-08-777-192-48
; Sequence 48, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:

APPLICANT: BROEKERT, WILLEM F.
APPLICANT: CAMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARB & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 16..255
US-08-777-192-48

Alignment Scores:
Pred. No.: 9.24e-28 Length: 414
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-10 (1-50) x US-08-777-192-48 (1-414)

Qy 1 LysLeuCysGluArgSerSerglyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 106 AAGTTGTGCGAAAGGCCAAGTGGACATGCTCAGGAGTCTGTGGAACAATAACGCATGC 165

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 166 AAGAAATCAGTGCATTAACTTGAAGAACGACGATGGATCTTGGAACTATGCTCTCCCA 225

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 226 GCTCACAAAGTGTATCTGCTACTTTCCTTGT 255

Search completed: May 13, 2004, 12:19:39
Job time : 88 secs

Db 226 GCTCACAAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 15

US-08-971-982-48
; Sequence 48, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; CAMMUE, BRUNO P.A.
; OSBORN, RUPERT W.
; REES, SARAH B.
; TERRAS, FRANKY R.G.
; VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,982
; FILING DATE: 17-No. 6187904-1997
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-971-982-48

Alignment Scores:
Pred. No.: 9.24e-28 Length: 414
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 3 Gaps: 0

US-10-006-252A-10 (1-50) x US-08-971-982-48 (1-414)

QY 1 LysLeuCysGluArgSerSerGlyThrTyrValCysGlyAsnAsnAlaCys 20
Db 106 AAGTTGTGGGAAGCCCAAGTGGACATGTCAGGAGTCGTGGAACAATAACGCATGC 165
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGATCAGTCAGTAATACCTTTGAGAAACACGACATGATCTTGCACACTATGCTTTCCCA 225
QY 41 AlaHisLysCysIleCysTyrPheProCys 50

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 13, 2004, 11:00:48 ; Search time 3321 Seconds
(without alignments)
68.324 Million cell updates/sec

Title: US-10-006-252A-10

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2947324 segs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosu62
-TRANS=human40.cddi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10006252 @CGN 1 1 333 @runat.11052004.141949.11000
-NCPU=6 -ICPU=3 -NO_WMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIME=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
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13: /cgn2_6/ptodata/1/pubpna/US09_PUB.seq:
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
17: /cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq:
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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ALIGNMENTS

RESULT 1
US-09-829-381A-17
; Sequence 17, Application US/09829381A
; Patent No. US2002014306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles B. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US2002014306A1h
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-829-381A-17

Alignment Scores:
Pred. No.: 6.96e-31 Length: 285
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservative: 2
Best Local Similarity: 92.00% Mismatches: 2
Query Match: 93.36% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-829-381A-17 (1-285)

Qy 1 LysLeuCySGluAArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCGAAAGGCCATCAGGACTTGGTCAGGAGTCTGGCGAAACACACACGCATGC 180
Qy 21 LysAsnGlnCysIleAArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCAATGCATCAGACTCGAAGGCGACGGCATGATCTTGCACTACGCTCTTCCCA 240
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

RESULT 2

US-10-681-972-17
Sequence 17, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yinnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyseum and Methods for Control
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
PRIOR FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 285
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Synthetic
US-10-681-972-17

Alignment Scores:
Pred. No.: 6.96e-31 Length: 285
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservative: 2
Best Local Similarity: 92.00% Mismatches: 2
Query Match: 93.36% Indels: 0
DB: 13 Gaps: 0

US-10-006-252A-10 (1-50) x US-10-681-972-17 (1-285)

Qy 1 LysLeuCySGluAArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 121 AAGTTGTGCGAAAGGCCATCAGGACTTGGTCAGGAGTCTGGCGAAACACACACGCATGC 180
Qy 21 LysAsnGlnCysIleAArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 181 AAGAACCAATGCATCAGACTCGAAGGCGACGGCATGATCTTGCACTACGCTCTTCCCA 240
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

RESULT 3

US-09-759-584-58
Sequence 58, Application US/09759584
Patent No. US20010014732A1
GENERAL INFORMATION:
APPLICANT: BROEKERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEVDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS

LOCATION: 43...282
US-09-759-584-58

Alignment Scores:

Pred. No.: 7.06e-31 Length: 288
Score: 281.00 Matches: 46
Percent Similarity: 96.00% Conservative: 2
Best Local Similarity: 92.00% Mismatches: 2
Query Match: 93.36% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-759-584-58 (1-288)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 133 AGTTGTGCCAAGGCCAAGTGGACATGCTCAGGAGTCTGTGGAAACATTAACGATGC 192
Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 193 AAGAATCAGTGCATTAGACTTGAGAAAGCAGCATGGATCTTGCAACTATGTCTTCCCA 252
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 253 GCTCAAGTGTACTCTGCTACTTCTCTTGT 282

RESULT 4

US-09-829-381A-5
; Sequence 5, Application US/09829381A
; Patent No. US20020144306A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, B54F
; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-829-381A-5

Alignment Scores:

Pred. No.: 7.7e-31 Length: 308
Score: 281.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 93.36% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-829-381A-5 (1-308)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGCGAGAGTCCAAAGTGGAAACATGCTCAGGCGTGTGGAAACAAACAATGCTTGC 218
Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 219 AAGAATCAGTGCATTAACTTGAAGAGCNCGACATGGATCTTGCAACTATGTCTTCCCA 278
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 279 GCTCAAGTGCATATGCTACTTCCGCTGT 308

RESULT 5

US-10-681-972-5
; Sequence 5, Application US/10681972
; Publication No. US20040064850A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide from Alyssum and Methods for Co
; Controlling Plant Pathogenic Fungi
; TITLE OF INVENTION: Antifungal Polypeptide from Alyssum and Methods for Co
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/10/681,972
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 308
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: Synthetic PCR reaction product
; OTHER INFORMATION: Synthetic PCR reaction product
; NAME/KEY: misc_feature
; LOCATION: (22)..(248)
; OTHER INFORMATION: N = any nucleotide

US-10-681-972-5

Alignment Scores:

Pred. No.: 7.7e-31 Length: 308
Score: 281.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 93.36% Indels: 0
DB: 13 Gaps: 0

US-10-006-252A-10 (1-50) x US-10-681-972-5 (1-308)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGCGAGAGTCCAAAGTGGAAACATGCTCAGGCGTGTGGAAACAAACAATGCTTGC 218
Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 219 AAGAATCAGTGCATTAACTTGAAGAGCNCGACATGGATCTTGCAACTATGTCTTCCCA 278
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 279 GCTCACAAGTGCATATGCTACTTCCCTGT 308

RESULT 6

US-09-829-381A-16
 ; Sequence 16, Application US/09829381A
 ; Patent No. US20020144306A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liang, Jihong
 ; APPLICANT: Shah, Dilip M.
 ; APPLICANT: Wu, Yonnie S.
 ; APPLICANT: Rosenberger, Cindy A.
 ; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
 ; Controlling Plant Pathogenic Fungi
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
 ; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
 ; CITY: St. Louis
 ; STATE: Missouri
 ; COUNTRY: USA
 ; ZIP: 63198

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/829,381A
 ; FILING DATE: 09-Apr-2001
 ; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/103,489

FILING DATE: 1998-06-24

ATTORNEY/AGENT INFORMATION:

NAME: Cohen, Charles E.

REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21 (10700)A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 537-6224

TELEFAX: (314) 537-6047

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 285 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid

DESCRIPTION: /desc = "synthetic DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-829-381A-16

Alignment Scores:

Pred. No.: 1.34e-30 Length: 285

Score: 279.00 Matches: 46

Percent Similarity: 94.00% Conservative: 1

Best Local Similarity: 92.00% Mismatches: 3

Query Match: 92.69% Indels: 0

DB: Gaps: 0

US-10-006-252A-10 (1-50) x US-09-829-381A-16 (1-285)

Qy 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 121 AAGTTGCGAGAGGCCATCAGGACTTGTCTGAGGAGTCTGCGGAAACAAACACCGCATGC 180

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 181 AAGAACCAATGCATCAACCTCGAGAGGCGCAGCATGCTTGCACACTACGTTCTTCCCA 240

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

US-09-829-381A-16

Alignment Scores:

Pred. No.: 1.34e-30 Length: 285

Score: 279.00 Matches: 46

Percent Similarity: 94.00% Conservative: 1

Best Local Similarity: 92.00% Mismatches: 3

Query Match: 92.69% Indels: 0

DB: Gaps: 0

US-10-006-252A-10 (1-50) x US-09-829-381A-16 (1-285)

Qy 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 121 AAGTTGCGAGAGGCCATCAGGACTTGTCTGAGGAGTCTGCGGAAACAAACACCGCATGC 180

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 181 AAGAACCAATGCATCAACCTCGAGAGGCGCAGCATGCTTGCACACTACGTTCTTCCCA 240

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

US-09-829-381A-16

RESULT 7

US-10-681-972-16
 ; Sequence 16, Application US/10681972
 ; Publication No. US20040064850A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liang, Jihong
 ; APPLICANT: Shah, Dilip M.
 ; APPLICANT: Wu, Yonnie S.
 ; APPLICANT: Rosenberger, Cindy A.
 ; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
 ; FILE REFERENCE: 38-21 (10700) C
 ; CURRENT APPLICATION NUMBER: US/10/681,972
 ; PRIOR FILING DATE: 2003-10-09
 ; PRIOR APPLICATION NUMBER: US/09/829,381D
 ; PRIOR FILING DATE: 2001-04-09
 ; PRIOR APPLICATION NUMBER: 09/103,489
 ; PRIOR FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 285
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 ; US-10-681-972-16

Alignment Scores:

Pred. No.: 1.34e-30 Length: 285

Score: 279.00 Matches: 46

Percent Similarity: 94.00% Conservative: 1

Best Local Similarity: 92.00% Mismatches: 3

Query Match: 92.69% Indels: 0

DB: Gaps: 0

US-10-006-252A-10 (1-50) x US-10-681-972-16 (1-285)

Qy 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 121 AAGTTGCGAGAGGCCATCAGGACTTGTCTGAGGAGTCTGCGGAAACAAACACCGCATGC 180

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 181 AAGAACCAATGCATCAACCTCGAGAGGCGCAGCATGCTTGCACACTACGTTCTTCCCA 240

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

US-09-759-584-48

Alignment Scores:

Pred. No.: 1.34e-30 Length: 285

Score: 279.00 Matches: 46

Percent Similarity: 94.00% Conservative: 1

Best Local Similarity: 92.00% Mismatches: 3

Query Match: 92.69% Indels: 0

DB: Gaps: 0

US-10-006-252A-10 (1-50) x US-09-759-584-48

Qy 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 121 AAGTTGCGAGAGGCCATCAGGACTTGTCTGAGGAGTCTGCGGAAACAAACACCGCATGC 180

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 181 AAGAACCAATGCATCAACCTCGAGAGGCGCAGCATGCTTGCACACTACGTTCTTCCCA 240

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

US-09-759-584-48

Alignment Scores:

Pred. No.: 1.34e-30 Length: 285

Score: 279.00 Matches: 46

Percent Similarity: 94.00% Conservative: 1

Best Local Similarity: 92.00% Mismatches: 3

Query Match: 92.69% Indels: 0

DB: Gaps: 0

US-10-006-252A-10 (1-50) x US-09-759-584-48

Qy 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 121 AAGTTGCGAGAGGCCATCAGGACTTGTCTGAGGAGTCTGCGGAAACAAACACCGCATGC 180

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 181 AAGAACCAATGCATCAACCTCGAGAGGCGCAGCATGCTTGCACACTACGTTCTTCCCA 240

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

US-09-759-584-48

Alignment Scores:

Pred. No.: 1.34e-30 Length: 285

Score: 279.00 Matches: 46

Percent Similarity: 94.00% Conservative: 1

Best Local Similarity: 92.00% Mismatches: 3

Query Match: 92.69% Indels: 0

DB: Gaps: 0

US-10-006-252A-10 (1-50) x US-09-759-584-48

Qy 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 121 AAGTTGCGAGAGGCCATCAGGACTTGTCTGAGGAGTCTGCGGAAACAAACACCGCATGC 180

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 181 AAGAACCAATGCATCAACCTCGAGAGGCGCAGCATGCTTGCACACTACGTTCTTCCCA 240

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

US-09-759-584-48

Alignment Scores:

Pred. No.: 1.34e-30 Length: 285

Score: 279.00 Matches: 46

Percent Similarity: 94.00% Conservative: 1

Best Local Similarity: 92.00% Mismatches: 3

Query Match: 92.69% Indels: 0

DB: Gaps: 0

US-10-006-252A-10 (1-50) x US-09-759-584-48

Qy 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 121 AAGTTGCGAGAGGCCATCAGGACTTGTCTGAGGAGTCTGCGGAAACAAACACCGCATGC 180

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 181 AAGAACCAATGCATCAACCTCGAGAGGCGCAGCATGCTTGCACACTACGTTCTTCCCA 240

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

US-09-759-584-48

Alignment Scores:

Pred. No.: 1.34e-30 Length: 285

Score: 279.00 Matches: 46

Percent Similarity: 94.00% Conservative: 1

Best Local Similarity: 92.00% Mismatches: 3

Query Match: 92.69% Indels: 0

DB: Gaps: 0

US-10-006-252A-10 (1-50) x US-09-759-584-48

Qy 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 121 AAGTTGCGAGAGGCCATCAGGACTTGTCTGAGGAGTCTGCGGAAACAAACACCGCATGC 180

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 181 AAGAACCAATGCATCAACCTCGAGAGGCGCAGCATGCTTGCACACTACGTTCTTCCCA 240

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

US-09-759-584-48

Alignment Scores:

Pred. No.: 1.34e-30 Length: 285

Score: 279.00 Matches: 46

Percent Similarity: 94.00% Conservative: 1

Best Local Similarity: 92.00% Mismatches: 3

Query Match: 92.69% Indels: 0

DB: Gaps: 0

US-10-006-252A-10 (1-50) x US-09-759-584-48

Qy 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 121 AAGTTGCGAGAGGCCATCAGGACTTGTCTGAGGAGTCTGCGGAAACAAACACCGCATGC 180

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 181 AAGAACCAATGCATCAACCTCGAGAGGCGCAGCATGCTTGCACACTACGTTCTTCCCA 240

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

US-09-759-584-48

Alignment Scores:

Pred. No.: 1.34e-30 Length: 285

Score: 279.00 Matches: 46

Percent Similarity: 94.00% Conservative: 1

Best Local Similarity: 92.00% Mismatches: 3

Query Match: 92.69% Indels: 0

DB: Gaps: 0

US-10-006-252A-10 (1-50) x US-09-759-584-48

Qy 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 121 AAGTTGCGAGAGGCCATCAGGACTTGTCTGAGGAGTCTGCGGAAACAAACACCGCATGC 180

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 181 AAGAACCAATGCATCAACCTCGAGAGGCGCAGCATGCTTGCACACTACGTTCTTCCCA 240

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

US-09-759-584-48

Alignment Scores:

Pred. No.: 1.34e-30 Length: 285

Score: 279.00 Matches: 46

Percent Similarity: 94.00% Conservative: 1

Best Local Similarity: 92.00% Mismatches: 3

Query Match: 92.69% Indels: 0

DB: Gaps: 0

US-10-006-252A-10 (1-50) x US-09-759-584-48

Qy 1 LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 121 AAGTTGCGAGAGGCCATCAGGACTTGTCTGAGGAGTCTGCGGAAACAAACACCGCATGC 180

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 181 AAGAACCAATGCATCAACCTCGAGAGGCGCAGCATGCTTGCACACTACGTTCTTCCCA 240

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270

US-09-759-584-48

Alignment Scores:

Pred. No.: 1.34e-30 Length: 285

Score: 279.00 Matches: 46

Percent Similarity: 94.00% Conservative: 1


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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,584
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/377,687
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
; US-09-759-584-48

Alignment Scores:
Pred. No.: 2,19e-30 Length: 414
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-759-584-48 (1-414)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 106 AAGTTGTCGAAAGCCAAAGTCGACATGTCAGGAGTCTGTGGAACATATACGCATGC 165
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
DB 166 AAGATCAGTCAGTAACTTGAAGAGCAGACATGATCTTGCAACTATGCTCTCCCA 225
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
DB 226 GCTCACAAGTGTATCTGCTACTTCTCTGT 255

RESULT 9
US-10-388-361A-45
; Sequence 45, Application US/10388361A
; Publication No. US20030226169A1
; GENERAL INFORMATION:
; APPLICANT: Van Amerongen, Aart
; APPLICANT: Fant, Franky
; APPLICANT: Borremans, Frans
; APPLICANT: De Samblaux, Genoveva
; APPLICANT: Sijtsma, Lolke
; APPLICANT: Mejoen, Robbert
; APPLICANT: Puijk, Wouter
; APPLICANT: Schaaper, Wilhelmus
; APPLICANT: Broekaert, Willem
; APPLICANT: Van Gelder, Wilhelmus
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: 50094PPDIV
; CURRENT APPLICATION NUMBER: US/10/388,361A
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 09/077,948
; PRIOR FILING DATE: 1998-08-07

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; PRIOR APPLICATION NUMBER: PCT/GB96/03068
; PRIOR FILING DATE: 1996-12-12
; PRIOR APPLICATION NUMBER: GB 9605552.9
; PRIOR FILING DATE: 1996-03-28
; PRIOR APPLICATION NUMBER: GB 9525455.3
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Raphanus sativus
; US-10-388-361A-45

Alignment Scores:
Pred. No.: 2,19e-30 Length: 414
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 13 Gaps: 0

US-10-006-252A-10 (1-50) x US-10-388-361A-45 (1-414)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 106 AAGTTGTCGAAAGCCAAAGTCGACATGTCAGGAGTCTGTGGAACATATACGCATGC 165
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
DB 166 AAGATCAGTCAGTAACTTGAAGAGCAGACATGATCTTGCAACTATGCTCTCCCA 225
QY 41 AlaHisLysCysIleCysTyrPheProCys 50
DB 226 GCTCACAAGTGTATCTGCTACTTCTCTGT 255

RESULT 10
US-10-006-252A-19
; Sequence 19, Application US/10006252A
; Publication No. US20020152498A1
; GENERAL INFORMATION:
; APPLICANT: De Samblaux, Genoveva
; APPLICANT: Broekaert, Willem
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: SYN-034DV
; CURRENT APPLICATION NUMBER: US/10/006,252A
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/077,951
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: GB 9525474.4
; PRIOR FILING DATE: 1995-12-13
; PRIOR APPLICATION NUMBER: PCT/GB96/03065
; PRIOR FILING DATE: 1996-12-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Raphanus sativus
; US-10-006-252A-19

Alignment Scores:
Pred. No.: 2,19e-30 Length: 414
Score: 279.00 Matches: 46
Percent Similarity: 94.00% Conservative: 1
Best Local Similarity: 92.00% Mismatches: 3
Query Match: 92.69% Indels: 0
DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x US-10-006-252A-19 (1-414)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

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Db 106 AAGTTGTCGGAAGCCCAAGTGGACATGCTGAGGAGTCTGTGGAACAACTAACGCATGC 165
Qy 21 LysAsnGlnCysIleA-gLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 166 AAGATCAGTGCATTAACTTGAAGAAGCAGCATGATCTTGCAACTATGTCTTCCCA 225
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 11

US-09-732-561-13
; Sequence 13, Application US/09732561
; Patent No. US20020035738A1
; GENERAL INFORMATION:
; APPLICANT: Thomma, Bart
; APPLICANT: Terras, Franky
; APPLICANT: Penninckx, Iris
; APPLICANT: Mannens, John
; APPLICANT: Kazan, Kemal
; APPLICANT: Broekaert, Willem
; TITLE OF INVENTION: Plant Protection Method
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Ag Products
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/202,638
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCV/GB97/01672
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: PPD 50165/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; STRAIN: PFD 1.1
; US-09-732-561-13

Alignment Scores:
Pred. No.: 1,09e-29 Length: 403
Score: 274.00 Matches: 45
Percent Similarity: 94.00% Conservative: 2
Best Local Similarity: 90.00% Mismatches: 3
Query Match: 91.03% Indels: 0
Gaps: 0
DB:

US-10-006-252A-10 (1-50) x US-09-732-561-13 (1-403)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 116 AAGTTGTCGAGAGGCAAGTGGACATGCTCGGAGTTTGGGAAACAGTAACGCGTGC 175
Qy 21 LysAsnGlnCysIleA-gLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 176 AAGAATCAGTGCATTAACTTGAAGAAGCAGCATGATCTTGCAACTATGTCTTCCCA 235
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 236 GCTCACAAGTGTATCTGCTACTTTCCTTGT 265

RESULT 12

US-09-938-842A-2046
; Sequence 2046, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2046
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-2046

Alignment Scores:

Pred. No.: 1.08e-29 Length: 243
Score: 272.00 Matches: 44
Percent Similarity: 94.00% Conservative: 3
Best Local Similarity: 88.00% Mismatches: 3
Query Match: 90.37% Indels: 0
Gaps: 0
DB:

US-10-006-252A-10 (1-50) x US-09-938-842A-2046 (1-243)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 91 AAGTTGTCGAGAGGCAAGTGGACATGCTCGGAGTTTGGGAAACAGTAATGTCATGC 150
Qy 21 LysAsnGlnCysIleA-gLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 151 AAGAATCAGTGCATTAACTTGAAGAAGCAGCATGATCTTGCAACTATGTCTTCCCA 210
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 211 GCACACAAGTGTATCTGCTACTTTCCTTGT 240

RESULT 13

US-09-938-842A-2046
; Sequence 2046, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2046
; LENGTH: 243
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2046

Alignment Scores:
Pred. No.: 1,08e-29 Length: 243
Score: 272.00 Matches: 44
Percent Similarity: 94.00% Conservative: 3
Best Local Similarity: 88.00% Mismatches: 3
Query Match: 90.37% Indels: 0
DB: 11 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-938-842A-2046 (1-243)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 91 AAGTTGTCGAGAGCAAGTGGACATGTCAGGGGTTTGGCGAAACAGTAATGATGC 150
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
DB 151 AAGAAATCAGTGCAATTAACCTTGAAGGAGCCAAACATGGATCATGCAACTATGTCCTCCA 210
QY 41 AlahisLysCysIleCysTyrPheProCys 50
DB 211 GCACACAAGTGATCTGTTACGTCCTCATGT 240

RESULT 14
US-09-732-561-15
; Sequence 15, Application US/09732561
; Patent No. US20020035738A1
; GENERAL INFORMATION:
; APPLICANT: Thoma, Bart
; APPLICANT: Terras, Franky
; APPLICANT: Penninckx, Iris
; APPLICANT: Manners, John
; APPLICANT: Kazan, Kemal
; APPLICANT: Broekaert, Willem
; TITLE OF INVENTION: Plant Protection Method
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Ag Products
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/202,638
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/01672
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:

; NAME: Hohenschurtz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: PPD 50165/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; STRAIN: PDF1.2
US-09-732-561-15

Alignment Scores:
Pred. No.: 2,08e-29 Length: 400
Score: 272.00 Matches: 44
Percent Similarity: 94.00% Conservative: 3
Best Local Similarity: 88.00% Mismatches: 3
Query Match: 90.37% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-732-561-15 (1-400)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
DB 122 AAGTTGTCGAGAGCAAGTGGACATGTCAGGGGTTTGGCGAAACAGTAATGATGC 181
QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
DB 182 AAGAAATCAGTGCAATTAACCTTGAAGGAGCCAAACATGGATCATGCAACTATGTCCTCCA 241
QY 41 AlahisLysCysIleCysTyrPheProCys 50
DB 242 GCACACAAGTGATCTGTTACGTCCTCATGT 271

RESULT 15
US-09-887-576-607
; Sequence 607, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US/09/887,576
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 607
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(400)
; OTHER INFORMATION: n = A, T, C or G
US-09-887-576-607
Alignment Scores:

Pred. No.: 2.08e-29 Length: 400
Score: 272.00 Matches: 44
Percent Similarity: 94.00% Conservative: 3
Best Local Similarity: 88.00% Mismatches: 3
Query Match: 90.37% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-10 (1-50) x US-09-887-576-607 (1-400)

Qy	1	LysLeuCysGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys	20
Db	122	AAATTGTGCGAGAGCCAAAGTGGACATGGTCAGGGGTTTGGGAAACAGTAATGCAATGC	181
Qy	21	LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro	40
Db	182	AAGAATCAGTGCATTAAACCTTGAAGGAGCCAAACATGGATCATGCACTATGTCTTCCCA	241
Qy	41	AlaHisLysCysIleCysTyrPheProCys	50
Db	242	GCACACAGGTGATCTGTACGTCCCATGT	271

Search completed: May 13, 2004, 13:15:13
Job time : 3323 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 13, 2004, 10:53:23 ; Search time 2518 Seconds
(without alignments)
592.974 Million cell updates/sec

Title: US-10-006-252A-10
Perfect score: 301
Sequence: 1 KLCRRSGTWSGVCNNAC.....QHGSNCYVFPAAKICVFFPC 50

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Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DGBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_hc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vit.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rtd.*
26: em_gss_phg.*
27: em_gss_vri.*
28: gb_gse1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	284	94.4	409	14	CD832294
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6	284	94.4	457	14	CD831226
7	284	94.4	473	14	CD834995
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9	284	94.4	476	14	CD834092
10	284	94.4	481	14	CD833924
11	284	94.4	482	14	CD833627
12	284	94.4	523	14	CD833661
13	284	94.4	543	14	CD828840
14	284	94.4	543	14	CD830628
15	284	94.4	646	14	CD829429
16	284	94.4	762	28	BZ517729
17	281	93.4	721	28	BH473290
18	280	93.0	522	14	CD833938
19	280	93.0	543	14	CD829085
20	279	92.7	408	14	CD833779
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30	279	92.7	438	14	CD831294
31	279	92.7	438	14	CD831479
32	279	92.7	446	14	CD834068
33	279	92.7	447	14	CD832592
34	279	92.7	450	14	CD834611
35	279	92.7	452	14	CD832071
36	279	92.7	453	14	CD834008
37	279	92.7	458	14	CD834994
38	279	92.7	470	14	CD831680
39	279	92.7	480	14	CD828332
40	279	92.7	553	14	CD831014
41	279	92.7	803	28	BH458392
42	276	91.7	727	28	BH940491
43	275	91.4	457	14	CD831392
44	274	91.0	358	9	AA713157
45	274	91.0	421	9	AV816118

ALIGNMENTS

RESULT 1
CA992140
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CA992140
HC0577 GIBCOBRL CAT. NO. 19643-014
CDNA, mRNA sequence.

346 bp
mRNA
linear
EST 10-OCT-2003
Brassica rapa subsp. pekinensis

GI:37621435

Brassica rapa subsp. pekinensis
Brassicaceae; Brassicaceae; Brassica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica

REFERENCE 1 (bases 1 to 346)
 AUTHORS Gao,R.J., Dai,D.P. and Ma,R.C.
 TITLE Expressed sequence tags of heading leaf during the heading process of Chinese cabbage
 JOURNAL Unpublished (2003)
 COMMENT Contact: Kongcai, Ma
 Plant Functional Genomics
 Beijing Agrobiotechnology Research Center
 Haidian District, Ban-Jing Rd., Beijing 100089, China
 Tel: 86 10 5150 3831
 Fax: 86 10 5150 3980
 Email: rcma@yahoo.com
 Seq primer: T7
 High quality sequence stop: 346
 POLYA=No.

FEATURES source
 1..346
 Location/Qualifiers
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="mRNA"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /tissue_type="heading leaf"
 /dev_stage="folding stage"
 /note="vector: pZLI; Site 1: NRI; Site 2: Sali; cDNA library was constructed by SUPERScriptTM Lambda System for cDNA Synthesis and Cloning (GIBCOBRL, CAT.NO.19643-014)"
 /clone_lib="GIBCOBRL CAT. NO. 19643-014"
 /lab_host="E.coli DH10B(Zip)"
 /note="vector: pZLI; Site 1: NRI; Site 2: Sali; cDNA library was constructed by SUPERScriptTM Lambda System for cDNA Synthesis and Cloning (GIBCOBRL, CAT.NO.19643-014)"

ORIGIN

Alignment Scores:
 Pred. No.: 6.8e-25 Length: 346
 Score: 301.00 Matches: 50
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CA992140 (1-346)

Qy 1 LysLeuCyGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 27 AAGTTGTCGAGAGTCAAGTGGGACATGCTCAGGAGTCTGTGAAACAAATACGCTGC 86
 Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 87 AAGATCATGTCATTCGACTTGAAGGAGCACACATGATGATGCACTATGTTCCCT 146
 Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 147 GCTCAAGTGTACTGTATTTCCTATG 176

RESULT 2
 CD832294
 LOCUS CD832294 409 bp mRNA linear EST 10-JUL-2003
 DEFINITION BN40.062L22F011227 BN40 Brassica napus cDNA clone BN40062L22, mRNA sequence.
 ACCESSION CD832294.1 GI:32514234
 VERSION CD832294.1
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 409)
 AUTHORS Genoplante.
 TITLE Genoplante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

FEATURES source
 Location/Qualifiers
 1..409
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN40062L22"
 /tissue_type="seed"
 /clone_lib="BN40"

ORIGIN

Alignment Scores:
 Pred. No.: 7.75e-23 Length: 409
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD832294 (1-409)

Qy 1 LysLeuCyGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 141 AAGCTGTGCGAAGGCCAAGTGGACGGTGGTCCAGAGTCTGTGAAACAAATATGCATGC 200
 Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 201 AAGAATCAGTGCATTCGACTAGAGAAAGCACACATGATCTTGCACATATGTTCTTCCCA 260
 Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 261 GCTCAAGTGCATTCGACTTTCCTTGT 290

RESULT 3

CD834852
 LOCUS CD834852 425 bp mRNA linear EST 10-JUL-2003
 DEFINITION BN45.043G08F011229 BN45 Brassica napus cDNA clone BN45043G08, mRNA sequence.
 ACCESSION CD834852
 VERSION CD834852.1 GI:32516792
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 425)
 AUTHORS Genoplante.
 TITLE Genoplante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

FEATURES source
 Location/Qualifiers
 1..425
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45043G08"
 /tissue_type="seed"
 /clone_lib="BN45"

ORIGIN

Alignment Scores:

Pred. No.: 8.18e-23 Length: 425
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD8334852 (1-425)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 139 AAGCTGTGCGAAAGCCCAAGTGGACGTCGTGAGAGTCGTGTGGAAACAATAATGATGCATGC 198
 Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 199 AAGATCAGTCATTCGACTAGAGAAAGCAGCATGGATCTTGGCAACTATGTCTTCCCA 258
 Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 259 GCTCACAAGTGCATCTGCTACTTCCCTTGT 288

RESULT 4

CD833613
 LOCUS BN40.067P16F011228 BN40 mRNA linear EST 10-JUL-2003
 DEFINITION 427 bp Brassica napus cDNA clone BN40067P16, mRNA

ACCESSION CD833613

VERSION CD833613.1 GI:32515553

KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM Brassica napus

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 JOURNAL rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (Bases 1 to 427)

REFERENCE

AUTHORS

TITLE Genoplatte, a major partnership french program in plant genomics

JOURNAL Unpublished (2003)

COMMENT Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>

and <http://genoplatte-info.infobiogen.fr>).

FEATURES

source

Location/Qualifiers
 1..427
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN40067P16"
 /tissue_type="seed"
 /clone_lib="BN40"

ORIGIN

Alignment Scores:
 Pred. No.: 8.23e-23 Length: 427
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD833613 (1-427)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 141 AAGCTGTGCGAAAGCCCAAGTGGACGTCGTGAGAGTCGTGTGGAAACAATAATGATGCATGC 200
 Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 201 AAGATCAGTCGATTCGACTAGAGAAAGCAGCATGGATCTTGGCAACTATGTCTTCCCA 260
 Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 261 GCTCACAAGTGCATCTGCTACTTCCCTTGT 290

RESULT 5

CD833047

LOCUS BN40.065M05F011229 BN40 mRNA linear EST 10-JUL-2003

DEFINITION 449 bp Brassica napus cDNA clone BN40065M05, mRNA

ACCESSION CD833047

VERSION CD833047.1 GI:32514987

KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (Bases 1 to 449)

REFERENCE

AUTHORS

TITLE Genoplatte, a major partnership french program in plant genomics

JOURNAL Unpublished (2003)

COMMENT Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>

and <http://genoplatte-info.infobiogen.fr>).

FEATURES

source

Location/Qualifiers
 1..449
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN40065M05"
 /tissue_type="seed"
 /clone_lib="BN40"

ORIGIN

Alignment Scores:
 Pred. No.: 8.82e-23 Length: 449
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD833047 (1-449)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 Db 122 AAGCTGTGCGAAAGCCCAAGTGGACGTCGTGAGAGTCGTGTGGAAACAATAATGATGCATGC 181

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 Db 182 AAGATCAGTCGATTCGACTAGAGAAAGCAGCATGGATCTTGGCAACTATGTCTTCCCA 241

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
 Db 242 GCTCACAAGTGCATCTGCTACTTCCCTTGT 271

RESULT 6

CD831226

LOCUS BN40.058J10F011019 BN40 mRNA linear EST 10-JUL-2003

DEFINITION 457 bp Brassica napus cDNA clone BN40058J10, mRNA

ACCESSION CD831226

VERSION CD831226.1 GI:32513166

KEYWORDS EST.

SOURCE Brassica napus (rape)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 457)
AUTHORS
TITLE Genoplahte, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplahte
Genoplahte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplahte' (<http://www.genoplahte.com>
and <http://genoplahte-info.infobiogen.fr>).

FEATURES
source
1..457
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN4008J10"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN
Alignment Scores:
Pred. No.: 9,048-23 Length: 457
Score: 284.00 Matches: 47
Percent Similarity: 96.00% Conservativity: 1
Best Local Similarity: 94.00% Mismatches: 2
Query Match: 94.35% Indels: 0
DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD831226 (1-457)

Qy 1 LysLeuCySGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 141 AAGTTGTGTGAGAGCCCAAGTGGGACATGTCAGGAGTTTGTGAAACAATAATGCGTGT 200
Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 201 AGAATCATGTCATTCGACTTGAGAAAGCAGCAGATGGAATCTTGCAACTATGTTCCCA 260
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 261 GCTCACAGTGTATCTGCTATTTCCCTGT 290

RESULT 7
CD834995
LOCUS CD834995 473 bp mRNA linear EST 10-JUL-2003
DEFINITION BN45.04308F011229 BN45 Brassica napus cDNA clone BN45043008, mRNA
sequence.
ACCESSION CD834995
VERSION CD834995.1 GI:32516935
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 473)
AUTHORS
TITLE Genoplahte, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplahte
Genoplahte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french

plant genomics programme 'Genoplahte' (<http://www.genoplahte.com>
and <http://genoplahte-info.infobiogen.fr>).

FEATURES
source
1..473
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45043008"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Alignment Scores:
Pred. No.: 9,498-23 Length: 473
Score: 284.00 Matches: 47
Percent Similarity: 96.00% Conservativity: 1
Best Local Similarity: 94.00% Mismatches: 2
Query Match: 94.35% Indels: 0
DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD834995 (1-473)

Qy 1 LysLeuCySGluArgSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
Db 159 AAGTTGTGTGAGAGCCCAAGTGGGACATGTCAGGAGTTTGTGAAACAATAATGCGTGT 218
Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
Db 219 AGAATCATGTCATTCGACTTGAGAAAGCAGCAGATGGAATCTTGCAACTATGTTCCCA 278
Qy 41 AlaHisLysCysIleCysTyrPheProCys 50
Db 279 GCTCACAGTGTATCTGCTATTTCCCTGT 308

RESULT 8
CD833784
LOCUS CD833784 476 bp mRNA linear EST 10-JUL-2003
DEFINITION BN45.001122F010914 BN45 Brassica napus cDNA clone BN45001122, mRNA
sequence.
ACCESSION CD833784
VERSION CD833784.1 GI:32515724
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 476)
AUTHORS
TITLE Genoplahte, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplahte
Genoplahte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplahte' (<http://www.genoplahte.com>
and <http://genoplahte-info.infobiogen.fr>).

FEATURES
source
1..476
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45001122"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Alignment Scores:
Pred. No.: 9,578-23 Length: 476

Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD833784 (1-476)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 |||||
 Db 160 AAGTTGTGTGAGAGGCCAAGTGGACATGGTCAGGAGTTTGTGGAACAATATGCGTGT 219
 |||||
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 |||||
 Db 220 AAGAATCAGTCATTCGACTTGAGAAAGCAGACATGGATCTTGCACACTATGCTTCCCA 279
 |||||
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 |||||
 Db 280 GCTCAAGTGTATCTGCTATTTCCCTTGT 309
 |||||

RESULT 9
 CD834092
 LOCUS
 DEFINITION BN45.040I23F011018 BN45 Brassica napus cDNA clone BN45040I23, mRNA
 sequence.
 ACCESSION CD834092
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Brassica napus (rape)
 Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 476)
 Genoplatte, a major partnership french program in plant genomics
 Genoplatte.
 Unpublished (2003)
 Contact: Genoplatte
 Genoplatte
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>)
 and <http://genoplatte-info.infobiogen.fr>.

FEATURES

source
 1..476
 Location/Qualifiers
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45040I23"
 /tissue_type="seed"
 /clone_lib="BN45"

ORIGIN

Alignment Scores:
 Pred. No.: 9.57e-23 Length: 476
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD834092 (1-476)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 |||||
 Db 160 AAGTTGTGTGAGAGGCCAAGTGGACATGGTCAGGAGTTTGTGGAACAATATGCGTGT 219
 |||||
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 |||||
 Db 220 AAGAATCAGTCATTCGACTTGAGAAAGCAGACATGGATCTTGCACACTATGCTTCCCA 279
 |||||

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 |||||
 Db 280 GCTCAAGTGTATCTGCTATTTCCCTTGT 309
 |||||

RESULT 10
 CD833924
 LOCUS
 DEFINITION BN45.040A03F011018 BN45 Brassica napus cDNA clone BN45040A03, mRNA
 sequence.
 ACCESSION CD833924
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Brassica napus (rape)
 Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 481)
 Genoplatte.
 Unpublished (2003)
 Contact: Genoplatte
 Genoplatte
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>)
 and <http://genoplatte-info.infobiogen.fr>.

FEATURES
 source
 1..481
 Location/Qualifiers
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45040A03"
 /tissue_type="seed"
 /clone_lib="BN45"

ORIGIN

Alignment Scores:
 Pred. No.: 9.71e-23 Length: 481
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD833924 (1-481)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 |||||
 Db 159 AAGTTGTGTGAGAGGCCAAGTGGACATGGTCAGGAGTTTGTGGAACAATATGCGTGT 218
 |||||
 QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 |||||
 Db 219 AAGAATCAGTCATTCGACTTGAGAAAGCAGACATGGATCTTGCACACTATGCTTCCCA 278
 |||||
 QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 |||||
 Db 279 GCTCAAGTGTATCTGCTATTTCCCTTGT 308
 |||||

RESULT 11
 CD833627
 LOCUS

DEFINITION BN45.001A11F010914 BN45 Brassica napus cDNA clone BN45001A11, mRNA
 sequence.
 ACCESSION CD833627
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Brassica napus (rape)
 Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 482)

Genoplante, a major partnership french program in plant genomics

Genoplante, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplante' (<http://www.genoplante.com>

and <http://genoplante-info.inbioogen.fr>).

FEATURES

source

1..482
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45001A11"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN

Alignment Scores:
Pred. No.: 9.74e-23 Length: 482
Score: 284.00 Matches: 47
Percent Similarity: 96.00% Conservative: 1
Best Local Similarity: 94.00% Mismatches: 2
Query Match: 94.35% Indels: 0
DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD833627 (1-482)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 160 AAGTTGTGTGAGAGCCNAGTGGACATGTCAGAGTTTGTGGAACAAATATGGTGT 219

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 220 AAGATCATGTCATTCGACTTGAAGAGCAGACATGATCTTGCAACTATGTTCTTCCA 279

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 280 GCTCACAAGTGTATCTGCTATTTCCCTTGT 309

RESULT 12

CD833661

LOCUS

BN45.001C04F010914 BN45 Brassica napus CDNA clone BN45001C04, mRNA

sequence.

ACCESSION CD833661

VERSION CD833661.1 GI:32515601

KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 523)

Genoplante, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplante' (<http://www.genoplante.com>

and <http://genoplante-info.inbioogen.fr>).

FEATURES

source

1..523
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45001C04"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN

Alignment Scores:
Pred. No.: 1.09e-22 Length: 523
Score: 284.00 Matches: 47
Percent Similarity: 96.00% Conservative: 1
Best Local Similarity: 94.00% Mismatches: 2
Query Match: 94.35% Indels: 0
DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD833661 (1-523)

Qy 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20

Db 142 AAGCTGTGCGAAGCCAAAGTGGACGTGTGAGAGTCTGTGGAAACAAATATGCAATGC 201

Qy 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40

Db 202 AAGAATCAGTGCATTCGACTAGAGAGCAGACATGATCTTGCAACTATGCTCTTCCA 261

Qy 41 AlaHisLysCysIleCysTyrPheProCys 50

Db 262 GCTCACAAGTGCATCTGCTACTTCCCTTGT 291

RESULT 13

CD828840

LOCUS

BN40.040A23F011019 BN40 Brassica napus cDNA clone BN40040A23, mRNA

sequence.

ACCESSION CD828840

VERSION CD828840.1 GI:32510780

KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 543)

Genoplante, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplante' (<http://www.genoplante.com>

and <http://genoplante-info.inbioogen.fr>).

and <http://genoplante-info.inbioogen.fr>).

FEATURES

source

1..543
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40040A23"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN

Alignment Scores:
Pred. No.: 1.15e-22 Length: 543
Score: 284.00 Matches: 47
Percent Similarity: 96.00% Conservative: 1

Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD828840 (1-543)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 |||||
 Db 141 AAGCTGTGCGAAGCGCAAGTGGACGTGTCAGGAGTCTGTGGAAACAATAATGATGC 200
 |||||

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 |||||
 Db 201 AAGATCAGTCGATTCGACTAGAGAAAGCACACATGGATCTTGCACACTATGCTTCCCA 260
 |||||

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 |||||

Db 261 GCTCAAGTGCATCTGCTACTTCCCTTGT 290
 |||||

RESULT 14
 CD830628
 LOCUS CD830628 543 bp mRNA linear EST 10-JUL-2003
 DEFINITION BN40.046D16F011221 BN40 Brassica napus cDNA clone BN40046D16, mRNA
 sequence.
 ACCESSION CD830628
 VERSION CD830628.1 GI:32512568
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 Genoplante.
 Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 CONTACT: Genoplante
 JOURNAL
 COMMENT

FEATURES
 source
 1..543
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN40046D16"
 /tissue_type="seed"
 /clone_lib="BN40"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.15e-22 Length: 543
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD830628 (1-543)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 |||||

Db 141 AAGCTGTGCGAAGCGCAAGTGGACGTGTCAGGAGTCTGTGGAAACAATAATGATGC 200
 |||||

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 |||||

Db 201 AAGATCAGTCGATTCGACTAGAGAAAGCACACATGGATCTTGCACACTATGCTTCCCA 260
 |||||

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 |||||

Db 261 GCTCAAGTGCATCTGCTACTTCCCTTGT 290
 |||||

RESULT 14
 CD830628
 LOCUS CD830628 543 bp mRNA linear EST 10-JUL-2003
 DEFINITION BN40.046D16F011221 BN40 Brassica napus cDNA clone BN40046D16, mRNA
 sequence.
 ACCESSION CD830628
 VERSION CD830628.1 GI:32512568
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 Genoplante.
 Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 CONTACT: Genoplante
 JOURNAL
 COMMENT

FEATURES
 source
 1..543
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN40046D16"
 /tissue_type="seed"
 /clone_lib="BN40"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.15e-22 Length: 543
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD830628 (1-543)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 |||||

Db 141 AAGCTGTGCGAAGCGCAAGTGGACGTGTCAGGAGTCTGTGGAAACAATAATGATGC 200
 |||||

Db 261 GCTCAAGTGCATCTGCTACTTCCCTTGT 290
 |||||

RESULT 15

CD829429

LOCUS CD829429 646 bp mRNA linear EST 10-JUL-2003

DEFINITION BN40.042B06F011226 BN40 Brassica napus cDNA clone BN40042B06, mRNA

sequence.

ACCESSION CD829429

VERSION CD829429.1 GI:32511369

KEYWORDS EST.

SOURCE Brassica napus (rape)

ORGANISM Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 Genoplante.
 Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 CONTACT: Genoplante
 JOURNAL
 COMMENT

FEATURES
 source
 1..646
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN40042B06"
 /tissue_type="seed"
 /clone_lib="BN40"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.46e-22 Length: 646
 Score: 284.00 Matches: 47
 Percent Similarity: 96.00% Conservative: 1
 Best Local Similarity: 94.00% Mismatches: 2
 Query Match: 94.35% Indels: 0
 DB: 14 Gaps: 0

US-10-006-252A-10 (1-50) x CD829429 (1-646)

QY 1 LysLeuCysGluArgSerSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys 20
 |||||

Db 135 AAGCTGTGCGAAGCGCAAGTGGACGTGTCAGGAGTCTGTGGAAACAATAATGATGC 194
 |||||

QY 21 LysAsnGlnCysIleArgLeuGluGlyAlaGlnHisGlySerCysAsnTyrValPhePro 40
 |||||

Db 195 AAGATCAGTCGATTCGACTAGAGAAAGCACACATGGATCTTGCACACTATGCTTCCCA 254
 |||||

QY 41 AlaHisLysCysIleCysTyrPheProCys 50
 |||||

Db 255 GCTCAAGTGCATCTGCTACTTCCCTTGT 284
 |||||

Search completed: May 13, 2004, 12:18:04

Job time : 2525 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: May 11, 2004, 16:57:25 ; Search time 59.5 Seconds
(without alignments)
3931.922 Million cell updates/sec

Title: US-10-006-252A-19

Perfect score: 752

Sequence: 1 gttttattagatcatggc.....caaaaaaaaaaaaaaaaaaaaa 414

Scoring table:

	BLOSUM62	Xgapop 10.0	Xgapext 0.5
Xgapop 10.0			
Xgapext 0.5			
Fgapop 6.0			
Delop 6.0			

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool.p/US10006252/runat.11052004.141656.22777/app_query.fasta.1.583
-DB=A Geneseq 29Jan04 -QPMT=fastan -SUFFIX=tag -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10006252.qcgn.1.81 @runat.11052004.141656.22777 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq 29Jan04.*

	1: Geneseq1980s.*
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3: Geneseq2000s.*	
4: Geneseq2001s.*	
5: Geneseq2002s.*	
6: Geneseq2003as.*	
7: Geneseq2003bs.*	
8: Geneseq2004s.*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	442	58.8	80	2 AAR33706	Aar33706 Antifunga
2	442	58.8	80	2 AAR57325	Aar57325 Antimicro
3	434	57.7	80	2 AAW19280	Aaw19280 Raphanus
4	434	57.7	80	2 AAW19617	Aaw19617 Radish an
5	433	57.6	80	2 AAR33708	Aar33708 Antifunga
6	433	57.6	80	2 AAR57327	Aar57327 Antimicro
7	432	57.4	80	7 ADC51222	Adc51222 Brassica
8	425	56.5	80	7 ADC51224	Adc51224 Brassica
9	423	56.2	80	3 AAY91117	Aay91117 Raphanus
10	418	55.6	187	3 AAY84072	Aay84072 Amino aci

11	417	55.5	80	4 AAB61792	Aab61792 Radish an
12	407	54.1	80	3 AAY57564	Aay57564 Wasabia j
13	407	54.1	80	5 ABP53725	Abp53725 Wasabia j
14	403	53.6	80	2 AAW40351	Aaw40351 A. thalia
15	403	53.6	80	2 AAW40346	Aaw40346 A. thalia
16	403	53.6	80	6 ABP81292	Abp81292 Arabidops
17	402	53.5	80	3 AAY57565	Aay57565 Wasabia j
18	402	53.5	80	5 ABP53726	Abp53726 Wasabia j
19	397	52.8	80	2 AAW40345	Aaw40345 A. thalia
20	397	52.8	80	4 AAB61794	Aab61794 Arabidops
21	395.5	52.7	79	2 AAW35560	Aaw35560 Alyssum s
22	359	47.7	607	3 AAG41694	Aag41694 Arabidops
23	309	41.1	51	2 AAW40349	Aaw40349 Radish Rs
24	309	41.1	51	2 AAY00738	Aay00738 Antifunga
25	309	41.1	51	4 AAB67417	Aab67417 Amino aci
26	309	41.1	51	4 AAB20220	Aab20220 Radish de
27	309	41.1	51	4 AAB49470	Aab49470 Radish an
28	309	41.1	51	4 AAB61793	Aab61793 White mus
29	307	40.8	149	3 AAY84060	Aay84060 Amino aci
30	304	40.4	50	4 AAE10625	Aae10625 Radish pl
31	304	40.4	51	2 AAW40347	Aaw40347 A. thalia
32	304	40.4	149	3 AAY70323	Aay70323 Dahlia me
33	304	40.4	149	3 AAY84058	Aay84058 Amino aci
34	302	40.2	51	2 AAW26372	Aaw26372 Radish an
35	302	40.2	51	2 AAW26374	Aaw26374 Radish an
36	301	40.0	51	2 AAW26371	Aaw26371 Radish an
37	301	40.0	157	3 AAY84066	Aay84066 Amino aci
38	301	40.0	360	3 AAY84067	Aay84067 Fusion pr
39	300	39.9	51	2 AAW19281	Aaw19281 Raphanus
40	300	39.9	51	2 AAW19616	Aaw19616 Radish an
41	300	39.9	51	2 AAW26375	Aaw26375 Radish an
42	300	39.9	51	2 AAY00737	Aay00737 Antifunga
43	300	39.9	51	4 AAB67416	Aab67416 Amino aci
44	300	39.9	51	4 AAB20221	Aab20221 Radish de
45	300	39.9	51	4 AAB49471	Aab49471 Radish an

ALIGNMENTS

RESULT 1
AAR33706
ID AAR33706 standard; protein; 80 AA.

AC AAR33706;

XX XX

DT 25-MAR-2003 (revised)

DT 07-JUL-1993 (first entry)

XX XX

DE Antifungal protein Rs-AFPI.

XX XX

Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
fungicide; bactericide; antibiotic; antifungal; gram positive;
plant disease resistance; low toxicity.

OS Raphanus sativus.

XX XX

PN WO3305153-A1.

XX XX

PD 18-MAR-1993.

XX XX

PF 27-AUG-1992; 92WO-GB001570.

XX XX

PR 29-AUG-1991; 91GB-00018523.

PR 13-FEB-1992; 92GB-00030308.

XX XX

25-JUN-1992; 92GB-00013526.

XX XX

PA (ICIL) IMPERIAL CHEM IND PLC.

XX XX

PI Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;

Vanderleyden J;

XX XX

DR WPI; 1993-100978/12.

XX XX

PT Biotic proteins isolated from seeds of plants - e.g. brassica or
PT dahlia, useful for increasing plants' resistance to fungal and bacterial
PT diseases.
XX
XX Disclosure; Fig 35; 110pp; English.
XX
XX This sequence is antifungal protein Rs-APF1 from Raphanus sativus. The
XX exact source and isolation of the encoding DNA sequence is unclear from
XX the specification. The protein is useful for combating fungi or bacteria
XX eg gram positive bacteria and plant pathogenic fungi. It has moderate
XX sensitivity to ions and an apparent low toxicity for cultured human
XX cells. Plants transformed with the encoding DNA show increased disease
XX resistance. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 80 AA;
SQ

Alignment Scores:
Pred. No.: 3,96e-40 Length: 80
Score: 442.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 58.78% Indels: 0
DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x AAR33706 (1-80)

QY 16 ATGGCTAAGTTTGGTCCATCGCACTTCTTTTGGCTCTTGTCTTTTGGCTGCT 75
DB 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAGCACCACAAATGGTGGAGCAGACAGAGTTGTGGAGGCGCAAGTGGACATGG 135
DB 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTGAAACAATAACGATGCAAGATCAGTGCATTAACTTGCAGAAAGCA 195
DB 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
QY 196 CGACATGATCTTCAACTATGCTTCCAGCTCAGAGTGCATCTGCTACTTTCCTTGT 255
DB 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 2
AAR57325
ID AAR57325 standard; protein; 80 AA.
XX
XX AAR57325;
XX
XX 25-MAR-2003 (revised)
DT 14-FEB-1995 (first entry)
XX
XX Antimicrobial Rs-APF1.
XX
XX Antimicrobial; Rs-APF1; symbiosis; disease-resistance; fungus-resistance;
KW Clavibacter xylia subsp. cynodontis; Cxc; crop improvement; endophyte.
XX
XX Raphanus sativus.
OS
XX
XX WO9416076-A1.
XX
XX 21-JUL-1994.
XX
XX 05-JAN-1994; 94WO-GB000012.
XX
XX 08-JAN-1993; 93GB-00000281.
XX
XX (ZENE) ZENECA LTD.
XX
XX DuBock AC, Powell KA, Rees SB;
XX
XX WPI; 1994-249223/30.
DR N-PSDB; AAQ70128.
XX

PT Antimicrobial protein producing endo-symbiotic microorganisms - is
PT produced by combining nucleic acids encoding the protein with an
PT endophyte, useful for protecting plant hosts from esp. fungal disease.
XX
XX Disclosure; Page 32; 39pp; English.
XX
XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
XX Clavibacter xylia subsp. cynodontis (Cxc). Plants or seeds treated with
XX recombinant Cxc are protected against fungal disease. A suitable
XX antimicrobial protein is Rs-APF1 from R. sativus. The full-length cDNA
XX sequence of Rs-APF1 is given in AAQ70128, and the amino acid sequence
XX predicted from this sequence in AAR57325. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX
XX Sequence 80 AA;
SQ

Alignment Scores:
Pred. No.: 3,96e-40 Length: 80
Score: 442.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 58.78% Indels: 0
DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x AAR57325 (1-80)

QY 16 ATGGCTAAGTTTGGTCCATCGCACTTCTTTTGGCTCTTGTCTTTTGGCTGCT 75
DB 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAGCACCACAAATGGTGGAGCAGACAGAGTTGTGGAGGCGCAAGTGGACATGG 135
DB 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTGAAACAATAACGATGCAAGATCAGTGCATTAACTTGCAGAAAGCA 195
DB 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
QY 196 CGACATGATCTTCAACTATGCTTCCAGCTCAGAGTGCATCTGCTACTTTCCTTGT 255
DB 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 3
AAR19280
ID AAR19280 standard; protein; 80 AA.
XX
XX AAR19280;
XX
XX 25-MAR-2003 (revised)
DT 19-JAN-1998 (first entry)
XX
XX Raphanus sativus antifungal protein 1 (Rs-APF1).
XX
XX Antifungal protein; candida; fungal resistance; food additive; radish;
KW crop protection; plant defensin; bacterial protection; preservative.
XX
XX Raphanus sativus.
OS
XX
XX Key Location/Qualifiers
XX Peptide 1..29
XX Protein 13..80
XX /label= antifungal protein_1
XX
XX Misc-difference 24
XX /note= "encoded by CCA"
XX
XX WO9721815-A2.
XX
XX 19-JUN-1997.
XX
XX 12-DEC-1996; 96WO-GB003068.
XX
XX 13-DEC-1995; 95GB-00025455.
XX
XX 28-MAR-1996; 96GB-00006552.
XX

XX (ZENE) ZENECA LTD.
 XX Meloen RH, Puijk WC, Schaaper WM, Sijtsma L, Van Amerongen A;
 PI Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB;
 PI Van Gelder WMJ;
 XX WPI; 1997-332786/30.
 DR N-PSDB; AAT72333.
 XX
 XX Antifungal peptide derived from radish antifungal protein 2 - and related
 PT DNA, useful for producing plants with increased fungal resistance and as
 PT therapeutic or preservative agent.
 XX
 XX Claim 1; Fig 2; 65pp; English.
 XX
 XX This protein sequence is a Raphanus sativus (radish) antifungal protein
 CC (RS-APPI). Analogues of the homologous protein, RS-APP2 (AAW19281), have
 CC also been produced (see AAW19282-92, AAW19294-98, AAW19301-04, AAW19330-
 CC 34 and AAW1765-83). Plants containing DNA sequences encoding these
 CC proteins have improved resistance to fungi. Compositions containing the
 CC peptides can be used to control fungi or bacteria in pharmaceutical (e.g.
 CC treatment of Candida infections) or preservative purposes (as food
 CC additives). In agriculture, the peptide may be used to improve disease
 CC resistance or disease tolerance of crops, either pre or post harvest.
 CC When applied to plants they may also have curative as well as protective
 CC actions. The peptides may also be used to protect plants by introducing
 CC them, or a microorganism capable of expressing the peptide into the soil.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 80 AA;

Alignment Scores:
 Pred. No.: 3,05e-39 Length: 80
 Score: 434.00 Matches: 79
 Percent Similarity: 98.75% Conservative: 0
 Best Local Similarity: 98.75% Mismatches: 1
 Query Match: 57.71% Indels: 0
 DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x AAW19280 (1-80)

QY 16 ATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTCTCTCTGTTCTTTTGTCTGCT 75
 Db 1 MetAlalysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaLa 20
 QY 76 TTCGAAGCACCAACAATGGTGGAGCACAGAGTTGTGGAAAGGCCAAGTGGGACATGG 135
 Db 21 PheGluAlaGluThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAAGTCAATTAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
 QY 196 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255
 Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 4
 AAW19617
 ID AAW19617 standard; protein; 80 AA.
 XX
 AC AAW19617;
 XX
 XX 13-DEC-1997 (first entry)
 DT
 DE Radish antifungal protein 1 (RS-APPI).
 XX

KW RS-APPI; radish antifungal protein 1; fungicide; salt tolerance;
 KW preservative; transgenic plant; crop protection.
 KW
 OS Raphanus sativus.
 XX

FH Key Location/Qualifiers
 FT Peptide 1..29
 FT /label= Pro-peptide
 FT Misc-difference 24
 FT /note= "encoded by CCA"
 FT Protein 30..80
 FT /label= Mat protein
 FT /note= "RsAFPI"
 XX
 XX WO9721814-A1.
 XX 19-JUN-1997.
 PD
 XX 12-DEC-1996; 96WO-GB003065.
 PF
 XX 13-DEC-1995; 95GB-00025474.
 PR
 XX (ZENE) ZENECA LTD.
 PA
 XX Broekaert WF, De Samblanx GW, Rees SB;
 PI
 XX WPI; 1997-332785/30.
 DR
 XX N-PSDB; AAT68696.
 XX
 XX New active mutants of radish antifungal protein 2 - used to generate
 PT fungus-resistant plants or as therapeutic or preservative agents.
 PT
 XX Disclosure; Fig 2; 39pp; English.

XX This polypeptide comprises the preprotein for radish antifungal protein 1
 CC (RS-APPI). Novel antifungal proteins are based on RS-APPI, RS-APP2 (see
 CC AAW19616), RS-APP3 and RS-APP4, especially those in which Gly9 is replaced
 CC by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by Met.
 CC Mutants (see AAW26371-90) of RS-APP2 are specifically claimed. The
 CC mutants show improved salt tolerant antifungal activity, particularly
 CC when expressed in plants
 XX

SQ Sequence 80 AA;

Alignment Scores:
 Pred. No.: 3,05e-39 Length: 80
 Score: 434.00 Matches: 79
 Percent Similarity: 98.75% Conservative: 0
 Best Local Similarity: 98.75% Mismatches: 1
 Query Match: 57.71% Indels: 0
 DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x AAW19617 (1-80)

QY 16 ATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTCTCTGTTCTTTTGTCTGCT 75
 Db 1 MetAlalysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaLa 20
 QY 76 TTCGAAGCACCAACAATGGTGGAGCACAGAGTTGTGGAAAGGCCAAGTGGGACATGG 135
 Db 21 PheGluAlaGluThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAAACAATAACGCATGCAAGAAATCAAGTCAATTAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
 QY 196 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255
 Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 5
 AAW19617
 ID AAW19617 standard; protein; 80 AA.
 XX
 AC AAW19617;
 XX
 XX 25-MAR-2003 (revised)
 DT
 DT 07-JUL-1993 (first entry)

XX Antifungal protein Rs-APP2.
 DE Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
 XX fungicide; bactericide; antibiotic; antifungal; gram positive;
 KW plant disease resistance; low toxicity.
 XX Raphanus sativus.
 OS WO9305153-A1.
 XX 18-MAR-1993.
 XX 27-AUG-1992; 92WO-GB001570.
 XX 29-AUG-1991; 91GB-00018523.
 XX 13-FEB-1992; 92GB-0003038.
 XX 25-JUN-1992; 92GB-00013526.
 XX (ICIL) IMPERIAL CHEM IND PLC.
 XX Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
 PI Vanderleyden J;
 XX WPI; 1993-100978/12.
 XX Biocidal proteins isolated from seeds of plants - e.g. brassica or
 PT dahlia, useful for increasing plants' resistance to fungal and bacterial
 PT diseases.
 XX Disclosure; Fig 35; 110pp; English.
 XX This sequence is part of antifungal protein Rs-APP2, decoded from a
 CC mutagenised RsAPP1 clone derived from Raphanus sativus. The protein is
 CC useful for combating fungi or bacteria eg gram positive bacteria and
 CC plant pathogenic fungi. It has moderate sensitivity to ions and an
 CC apparent low toxicity for cultured human cells. Plants transformed with
 CC the encoding DNA show increased disease resistance. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX SQ Sequence 80 AA;
 Alignment Scores:
 Pred. No.: 3,93e-39 Length: 80
 Score: 433.00 Matches: 78
 Percent Similarity: 98.75% Conservative: 1
 Best Local Similarity: 97.50% Mismatches: 1
 Query Match: 57.50% Indels: 0
 DB: 2 Gaps: 0
 US-10-006-252A-19 (1-414) x AAR33708 (1-80)
 QY 16 ATGGCTAAGTTTGGCTCCATCGCACTTCTTTTGTCTCTTTTGTCTTTTGTCTGCT 75
 Db 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaAla 20
 QY 76 TTCGAAGCACCACCAATGTGTGAAGCAGACAGAGTTGTGCGAAGGCCCAAGTGGACATGG 135
 Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAACAATAACCGCATCGCAAGATCAGTGCATTAACTTGAGGAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
 QY 196 CGACATGATCTTGAACATATGTCTTCCAGCTCACAAAGTGTATCTGCTACTTCTTGT 255
 Db 61 ArgHisGlySerCysAsnTyValPheProAlaHisLysCysIleCysTyrrPheProCys 80
 RESULT 6
 AAR57327
 ID AAR57327 standard; protein; 80 AA.
 XX AAR57327;
 AC AAR57327;

XX 25-MAR-2003 (revised)
 DT 14-FEB-1995 (first entry)
 XX Antimicrobial Rs-APP2.
 DE Antimicrobial; Rs-APP2; symbiosis; disease-resistance; fungus-resistance;
 XX Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte;
 KW PCR; polymerase chain reaction; mutagenesis.
 XX Raphanus sativus.
 OS WO9416076-A1.
 XX 21-JUL-1994.
 XX 05-JAN-1994; 94WO-GB000012.
 XX 08-JAN-1993; 93GB-00000281.
 XX (ZENE) ZENECA LTD.
 XX Dubock AC, Powell KA, Rees SB;
 XX WPI; 1994-249223/30.
 XX N-PSDB; AAQ70130.
 XX Antimicrobial protein producing endo-symbiotic microorganisms - is
 PT produced by combining nucleic acids encoding the protein with an
 PT endophyte, useful for protecting plant hosts from esp. fungal disease.
 XX Disclosure; Page 33-34; 39pp; English.
 XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
 CC Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with
 CC recombinant Cxc are protected against fungal disease. A suitable
 CC antimicrobial protein is Rs-APP1 from R. sativus. The full-length cDNA
 CC sequence of PCR assisted site-directed mutagenesis of Rs-APP2 is given in
 CC AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX SQ Sequence 80 AA;
 Alignment Scores:
 Pred. No.: 3,93e-39 Length: 80
 Score: 433.00 Matches: 78
 Percent Similarity: 98.75% Conservative: 1
 Best Local Similarity: 97.50% Mismatches: 1
 Query Match: 57.50% Indels: 0
 DB: 2 Gaps: 0
 US-10-006-252A-19 (1-414) x AAR57327 (1-80)
 QY 16 ATGGCTAAGTTTGGCTCCATCGCACTTCTTTTGTCTCTTTTGTCTTTTGTCTGCT 75
 Db 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaLeuValLeuPheAlaAla 20
 QY 76 TTCGAAGCACCACCAATGTGTGAAGCAGACAGAGTTGTGCGAAGGCCCAAGTGGACATGG 135
 Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAACAATAACCGCATCGCAAGATCAGTGCATTAACTTGAGGAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
 QY 196 CGACATGATCTTGAACATATGTCTTCCAGCTCACAAAGTGTATCTGCTACTTCTTGT 255
 Db 61 ArgHisGlySerCysAsnTyValPheProAlaHisLysCysIleCysTyrrPheProCys 80
 RESULT 7
 ADC51222
 ID ADC51222 standard; protein; 80 AA.
 XX


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AC ADC51222;
XX
XX 18-DEC-2003 (first entry)
XX
XX Brassica oleracea defensin protein.
XX
XX antimicrobial protein; defensin; transgenic plant;
XX composite disease resistance; pathogenic bacteria;
XX rice white leaf blight; brown-stripe disease; glume blight;
XX seedling damping-off disease; filamentous fungi; rice blight;
XX sheath blight disease; leaf blight.
XX Brassica oleracea.
XX OS
XX JP2003088379-A.
XX PN
XX 25-MAR-2003.
XX PD
XX 18-SEP-2001; 2001JP-00283117.
XX PF
XX 18-SEP-2001; 2001JP-00283117.
XX PR
XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX PA
XX WPI; 2003-621123/59.
XX DR N-PSDB; ADC51221.
XX
XX Novel protein from Brassica campestris, useful as antimicrobial against
XX plant pathogenic filamentous fungi or pathogenic bacteria, especially for
XX treating e.g. rice white leaf blight and sheath blight disease.
XX
XX Claim 1; SEQ ID NO 2; 34pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequences of
XX antimicrobial (defensin) proteins from Brassica. The DNA and protein
XX sequences of the invention are useful for producing transformed plants
XX with composite disease resistance, especially resistant to diseases
XX caused by pathogenic bacteria, such as: rice white leaf blight, brown-
XX stripe disease, glume blight, and seedling damping-off disease. As well
XX as diseases caused by filamentous fungi, such as: rice blight, sheath
XX blight disease, and leaf blight. The present amino acid sequence
XX represents a Brassica defensin protein of the invention.
XX
XX Sequence 80 AA;
XX
Alignment Scores:
Pred. No.: 5.07e-39 Length: 80
Score: 432.00 Matches: 78
Percent Similarity: 97.50% Conservative: 0
Best Local Similarity: 97.50% Mismatches: 2
Query Match: 57.45% Indels: 0
DB: 7 Gaps: 0
US-10-006-252A-19 (1-414) x ADC51222 (1-80)
QY 16 ATGGCTAAGTTGGTGGTCCATCGCAGCTCTTTTGGCTGCTGTTCTTTTCTGCTGCT 75
Db 1 MetAlaLysPheValSerIleIleAlaLeuPheAlaAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAGGACCAACATGGTGGAGCACAGAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
Db 21 LeuGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTGGAACAAATACGCATGCAGATCAGTGCATTAACTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
QY 196 CGACATGGATCTTGCAACTATGCTTCCAGCTCAAGTGTATCTGCTACTTTCCTTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80
RESULT 8
ADC51224

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ID ADC51224 standard; protein; 80 AA.
XX
XX ADC51224;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Brassica defensin protein.
DE
XX
XX antimicrobial protein; defensin; transgenic plant;
XX composite disease resistance; pathogenic bacteria;
XX rice white leaf blight; brown-stripe disease; glume blight;
XX seedling damping-off disease; filamentous fungi; rice blight;
XX sheath blight disease; leaf blight.
KW
XX Brassica sp.
OS
XX
XX JP2003088379-A.
XX PN
XX 25-MAR-2003.
XX PD
XX 18-SEP-2001; 2001JP-00283117.
XX PF
XX 18-SEP-2001; 2001JP-00283117.
XX PR
XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX PA
XX WPI; 2003-621123/59.
XX DR N-PSDB; ADC51223.
XX
XX Novel protein from Brassica campestris, useful as antimicrobial against
XX plant pathogenic filamentous fungi or pathogenic bacteria, especially for
XX treating e.g. rice white leaf blight and sheath blight disease.
XX
XX Claim 1; SEQ ID NO 4; 34pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequences of
XX antimicrobial (defensin) proteins from Brassica. The DNA and protein
XX sequences of the invention are useful for producing transformed plants
XX with composite disease resistance, especially resistant to diseases
XX caused by pathogenic bacteria, such as: rice white leaf blight, brown-
XX stripe disease, glume blight, and seedling damping-off disease. As well
XX as diseases caused by filamentous fungi, such as: rice blight, sheath
XX blight disease, and leaf blight. The present amino acid sequence
XX represents a Brassica defensin protein of the invention.
XX
XX Sequence 80 AA;
XX
Alignment Scores:
Pred. No.: 3.02e-38 Length: 80
Score: 425.00 Matches: 77
Percent Similarity: 96.25% Conservative: 0
Best Local Similarity: 96.25% Mismatches: 3
Query Match: 56.52% Indels: 0
DB: 7 Gaps: 0
US-10-006-252A-19 (1-414) x ADC51224 (1-80)
QY 16 ATGGCTAAGTTGGTGGTCCATCGCAGCTCTTTTGGCTGCTGTTCTTTTCTGCTGCT 75
Db 1 MetAlaLysPheValSerIleIleAlaLeuPheAlaAlaLeuValLeuAlaAla 20
QY 76 TTCGAGGACCAACATGGTGGAGCACAGAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTGGAACAAATACGCATGCAGATCAGTGCATTAACTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
QY 196 CGACATGGATCTTGCAACTATGCTTCCAGCTCAAGTGTATCTGCTACTTTCCTTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

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RESULT 9
RAY91117
ID  AAY91117 standard; protein; 80 AA.
XX
AC  AAY91117;
XX
DT  06-OCT-2000 (first entry)
XX
DE  Raphanus sativus antibacterial protein radishin SEQ ID NO:2.
XX
KW  Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;
XX  pathogenic microbe; radish; rice blast disease.
XX
OS  Raphanus sativus.
XX
PN  JP2000116379-A.
XX
PD  25-APR-2000.
XX
PF  09-OCT-1998; 98JP-00288472.
XX
PR  09-OCT-1998; 98JP-00288472.
XX
PA  (TOYA-) TOYAMA KEN.
XX
DR  WPI: 2000-389821/34.
XX  N-PSDB; AAA53190.
XX
PT  Isolated DNA from Raphanus sativus used to transform a microbe and a
PT  plant to produce an antibacterial protein used to increase resistance of
PT  rice paddy against pathogenic microbes.
XX
PS  Claim 5; Page 4-5; 7pp; Japanese.
XX
CC  The present sequence represents an antibacterial protein, designated
CC  radishin, isolated from Raphanus sativus (radish). A phage or plasmid
CC  comprising radishin can be used for increasing resistance of paddy and
CC  rice blast disease against pathogenic microbes
XX
SQ  Sequence 80 AA;

Alignment Scores:
Pred. No.: 5,04e-38 Length: 80
Score: 423.00 Matches: 75
Percent Similarity: 97.50% Conservative: 3
Best Local Similarity: 93.75% Mismatches: 2
Query Match: 56.25% Indels: 0
DB: 3 Gaps: 0

US-10-006-252A-19 (1-414) x RAY91117 (1-80)
Qy 16 ATGGCTAAGTTGGCTGCATCATGCACTTCTTTTCTGCTCTTGTCTTTTGTCTGTCT 75
Db 1 MetAlaLysPheAlaSerIleIleValLeuLeuPheAlaLeuValPheSerAla 20
Qy 76 TTCGAAGCACCACCAATGTGTGAAGCAGACAGAGTTGTGCAAGGCCAAGTGGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
Qy 136 TCAGGAGTCTGTGGAAACAAATAACGCATGCAAGAAATCAGTGCATTAACCTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
Qy 196 CGACATGGATCTTGCAACTATGCTCTCCAGCTCACAAAGTGTATCTGCTACTTCTCTTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 10
AAY84072
ID  AAY84072 standard; protein; 187 AA.
XX
AC  AAY84072;
XX
DT  03-JUL-2000 (first entry)
XX
DE  Amino acid sequence of a fusion protein of DmAMP1 and RsAPP2.
XX
KW  Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
XX  protein expression; plant defensin; RsAPP2; antifungal protein; APP2.
XX
OS  Synthetic.
XX  Dahlia merckii.
XX  Unidentified.
XX
FH  Key Location/Qualifiers
XX  Protein 29..78
XX  Peptide /note= "DmAMP1"
XX  Peptide 79..136
XX  Protein /note= "linker"
XX  Protein 137..187
XX  Protein /note= "RsAPP2"
XX
PN  WO200011175-A1.
XX
PD  02-MAR-2000.
XX
PF  17-AUG-1999; 99WO-GB002716.
XX
PR  18-AUG-1998; 98GB-00018001.
XX  04-DEC-1998; 98GB-00026753.
XX
PA  (ZENE ) ZENECA LTD.
XX
PI  Broekaert WF, Francois IEUA, De Bolle MFC, Evans IJ, Ray JA;
XX  WPI: 2000-246564/21.
XX  N-PSDB; AA299339.
XX
DR  Improving expression of polyproteins in plants involves coexpression of
DR  two or more proteins in plants within a single transcription unit.
XX
PS  Claim 33; Fig 34; 151pp; English.
XX
CC  The present sequence represents a protein of the invention, comprising
CC  the mature proteins of the plant defensins, the Dahlia antimicrobial
CC  protein (AMP) 1 and the antifungal protein 2 (RsAPP2), linked by a linker
CC  propeptide of the invention. The specification describes methods for
CC  improving expression levels of one or more proteins in a transgenic
CC  plant. The method comprises inserting a DNA sequence having a promoter
CC  region operably linked to two or more protein encoding regions separated
CC  by a DNA sequence coding for a linker propeptide and a terminator region.
CC  The method is used to produce proteins in plants. The linker propeptide
CC  comprising a cleavage site, whereby the expressed polypeptide is post-
CC  translationally processed into the component protein molecules. The
CC  propeptide sequence is rich in amino acids A, V, S and T and contains
CC  dipeptidic sequences consisting of either two acidic, two basic or one
CC  acidic and one basic residue as a cleavable linker sequence
XX
SQ  Sequence 187 AA;

Alignment Scores:
Pred. No.: 2.17e-37 Length: 187
Score: 418.00 Matches: 76
Percent Similarity: 96.25% Conservative: 1
Best Local Similarity: 95.00% Mismatches: 3
Query Match: 55.59% Indels: 0
DB: 3 Gaps: 0

US-10-006-252A-19 (1-414) x AAY84072 (1-187)
Qy 16 ATGGCTAAGTTGGCTGCATCATGCACTTCTTTTGTGCTCTTGTCTTTTGTCTGTCT 75
Db 108 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValPheAlaAla 127
Qy 76 TTCGAAGCACCACCAATGTGTGAAGCAGACAGAGTTGTGCAAGGCCAAGTGGGACATGG 135

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Db 128 PheGluAlaProThrWetValGluAlaGlnLysLeuCysGlnArgProSerArgThrTrp 147
QY 136 TCAGGAGTCTGGGAACAATAACCATGCGAAGTATGATGATTAACCTTGAGAAAGCA 195
Db 148 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAaGLeuGluLysAla 167
QY 196 CGACATGGAATCTGCAATATGCTCTTCCAGCTCACAAGTGTATCTCTACTTCTCTGT 255
Db 168 ArgHisGlySerCysAsnTyrArgPheProAlaHisLysCysIleCysTyrPheProCys 187

RESULT 11
AAB61792
ID AAB61792 standard; protein; 80 AA.
AC AAB61792;
XX
DT 20-APR-2001 (first entry)
XX
DE Radish antifungal defensin.
XX
KW Sunflower; anti-pathogenic; pathogenesis-related protein-5; PR5; BBE;
KW defensin; berberine bridge enzyme; plant pathogen; disease resistance;
KW agricultural; pharmaceutical; antifungal; antibacterial; antiviral;
KW antimicrobial; gene therapy; radish.
XX
OS Raphanus sativus.
XX
PN WO200078983-A2.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-US017090.
XX
PR 23-JUN-1999; 99US-0140646P.
PR 01-NOV-1999; 99US-0162904P.
PR 08-JUN-2000; 2000US-00589733.
XX
PA (PION-) PIONEER HI-BRED INT INC.
PA (CURA-) CURAGEN CORP.
XX
PI Bidney DL, Crasta OR, Duvick JP, Hu X, Lu G;
XX WPI; 2001-102729/11.
XX

Increasing pathogen (e.g. fungus, bacteria and virus) resistance in plants, comprises transforming plants with a DNA construct containing a nucleic acid sequence encoding anti-pathogenic proteins.
PS Disclosure; Fig 4; 86pp; English.
XX
CC The invention relates to sunflower anti-pathogenic proteins such as pathogenesis-related protein-5 (PR5), defensin and berberine bridge enzyme (BBE). DNA constructs containing nucleotide sequences encoding the anti-pathogenic proteins are useful for increasing resistance against pathogens e.g. fungal pathogen in monocot or dicot plants. The purified sunflower proteins (PR5, defensin or BBE) and compositions containing the proteins are useful for controlling plant pathogen by using procedures of spraying, dusting, scattering or seed coating, to the plants or the environment of the pathogen. The anti-pathogenic genes are useful as genetic markers in disease resistance breeding programs. Promoters capable of driving expression of the proteins are useful to express anti-pathogenic genes including disease and insect resistance genes. The proteins can also be used in agricultural and pharmaceutical compositions as antifungal and antimicrobial agents. The nucleotide sequences encoding the anti-pathogenic proteins are useful for transgenic plant production and for enhancing plant defense mechanism. The present sequence represents a radish antifungal defensin (Swiss-Pat Acn No. P30230), used in homology studies with sunflower defensin
SQ Sequence 80 AA;

Alignment Scores:
Pred. No.: 2.33e-37 Length: 80
Score: 407.00 Matches: 72
Percent Similarity: 96.25% Conservativeness: 5
Best Local Similarity: 90.00% Mismatches: 3
Query Match: 54.12% Indels: 0
DB: Gaps: 0

Score: 417.00 Matches: 74
Percent Similarity: 95.00% Conservativeness: 2
Best Local Similarity: 92.50% Mismatches: 4
Query Match: 55.45% Indels: 0
DB: Gaps: 0

US-10-006-252A-19 (1-414) x AAB61792 (1-80)
QY 16 ATGGCTAAGTTGGCTGCATCATCGCACTTCTTTTCTGCTCTGTTCTTTTCTGCTGT 75
Db 1 MetAlaLysPheAlaSerIleIleValLeuLeuPheValAlaLeuValPheAlaAla 20
QY 76 TTCGAGCACCACCAACAATGGTGGAGACACAGAAGTTGTGCAAGGCCAAAGTGGACATGG 135
Db 21 PheGluGluProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTGAAAACAATAACGCATGCAAGAATCAGTCGATTAACCTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
QY 196 CGACATGGAATCTGCAATATGCTCTTCCAGCTCACAAGTGTATCTCTACTTCTCTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 12
AAY57564
ID AAY57564 standard; protein; 80 AA.
XX
AC AAY57564;
XX
DT 12-SEP-2003 (revised)
DT 01-MAR-2000 (first entry)
XX
DE Wasabia japonica antibacterial protein SEQ ID NO:2.
XX
KW Wasabia japonica; antibacterial; food additive.
XX
OS Eutrema wasabi.
XX
PN JPI11313678-A.
XX
PD 16-NOV-1999.
XX
PF 30-APR-1998; 98JP-00121303.
XX
PR 30-APR-1998; 98JP-00121303.
XX
PA (IWAT-) IWATE KEN.
XX
DR WPI; 2000-057353/05.
DR N-PSDB; AAZ39123.
XX
PT An antibacterial protein gene of Wasabia japonica - useful as a food- or feed-additive.
XX
PS Claim 1; Page 13; 16pp; Japanese.
XX
CC The present sequence represents an antibacterial protein isolated from Wasabia japonica. The antibacterial protein can be used as a food or feed additive. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 80 AA;

Alignment Scores:
Pred. No.: 2.98e-36 Length: 80
Score: 407.00 Matches: 72
Percent Similarity: 96.25% Conservativeness: 5
Best Local Similarity: 90.00% Mismatches: 3
Query Match: 54.12% Indels: 0
DB: Gaps: 0

US-10-006-252A-19 (1-414) x AAY57564 (1-80)
US-10-006-252A-19 (1-414) x AAY57564 (1-80)

QY 16 ATGGCTAAGTTTGGTCCATCATCCGACCTCTTTTGTCTCTCTTGTCTTTTGTCTGCT 75
 Db 1 MetAlalysePheAlaSerIleIleAlaLeuPheAlaLeuValLeuPheSerAla 20
 QY 76 TTGGAAGCACCAATGCTGGAAGCACAGAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
 Db 21 PheGluAlaProSerMetValGluAlaGlnLysLeuCysGluLysSerSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAAACAATACGCAATCAGTGCATTAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
 QY 196 CGACATGGATCTTGCACATGCTCTCCAGCTCACAGTGTATCTGCTACTTCTCTTGT 255
 Db 61 ArgHisGlySerCysAsnTyrIlePheProTyrHisArgCysIleCysTyrPheProCys 80
 RESULT 13
 AAW53725
 ID ABP53725 standard; protein; 80 AA.
 XX AC AAW53725;
 XX DT 02-JUN-2003 (first entry)
 XX DE Wasabia japonica gamma-thionin protein SEQ ID NO:2.
 XX KW Wasabia japonica; gamma-thionin; plant; disease-resistant plant.
 XX OS Eutrema wasabi.
 XX PN JP2002272292-A.
 XX PD 24-SEP-2002.
 XX PF 22-MAR-2001; 2001JP-00083526.
 XX PR 22-MAR-2001; 2001JP-00083526.
 XX PA (IWAT-) IWATE KEN.
 XX DR WPI; 2002-718704/78.
 XX DR N-PSDB; ABQ82690.
 XX PT A disease-resistant plant in which wasabi gamma-thionin gene is introduced, creation of the disease-resistant plant.
 XX PS Claim 2; Page 8; 11pp; Japanese.
 CC The present invention describes a disease-resistant plant in which a wasabi gamma-thionin gene is introduced. Also described is a method for the creation of the above disease-resistant plant by introducing a wasabi gamma-thionin gene to a plant. The present sequence represents a Eutrema wasabi (Wasabia japonica) gamma-thionin protein from the present invention
 SQ Sequence 80 AA;
 Alignment Scores:
 Pred. No.: 2,98e-36 Length: 80
 Score: 407.00 Matches: 72
 Percent Similarity: 95.25% Conservative: 5
 Best Local Similarity: 90.00% Mismatches: 3
 Query Match: 54.12% Indels: 0
 DB: 5 Gaps: 0
 US-10-006-252A-19 (1-414) x ABP53725 (1-80)
 QY 16 ATGGCTAAGTTTGGTCCATCATCCGACCTCTTTTGTCTCTCTTGTCTTTTGTCTGCT 75
 Db 1 MetAlalysePheAlaSerIleIleAlaLeuPheAlaLeuValLeuPheSerAla 20
 QY 76 TTGGAAGCACCAATGCTGGAAGCACAGAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
 Db 21 PheGluAlaProSerMetValGluAlaGlnLysLeuCysGluLysSerSerGlyThrTrp 40

Db 21 PheGluAlaProSerMetValGluAlaGlnLysLeuCysGluLysSerSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAAACAATACGCAATCAGTGCATTAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
 QY 196 CGACATGGATCTTGCACATGCTCTCCAGCTCACAGTGTATCTGCTACTTCTCTTGT 255
 Db 61 ArgHisGlySerCysAsnTyrIlePheProTyrHisArgCysIleCysTyrPheProCys 80
 RESULT 14
 AAW40351
 ID AAW40351 standard; protein; 80 AA.
 XX AC AAW40351;
 XX DT 23-JUN-1998 (first entry)
 XX DE A. thaliana PDF1.2 protein.
 XX KW Defensein; PDF1.2; protection; plant; pathogen; jasmonate; ethylene; fungi.
 XX OS Arabidopsis thaliana.
 XX PN W09800023-A2.
 XX PD 08-JAN-1998.
 XX PF 20-JUN-1997; 97WO-CB001672.
 XX PR 01-JUL-1996; 96GB-00013753.
 XX PA (ZENE) ZENECA LTD.
 XX PI Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras FRG, Manners JM, Kazan K;
 XX DR WPI; 1998-086663/08.
 XX DR N-PSDB; AAV10646.
 XX PT Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.
 XX PS Claim 20; Fig 14; 72pp; English.
 CC This sequence represents an Arabidopsis PDF1.2 gene which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
 SQ Sequence 80 AA;
 Alignment Scores:
 Pred. No.: 8,26e-36 Length: 80
 Score: 403.00 Matches: 71
 Percent Similarity: 95.00% Conservative: 5
 Best Local Similarity: 88.75% Mismatches: 4
 Query Match: 53.59% Indels: 0
 DB: 2 Gaps: 0
 US-10-006-252A-19 (1-414) x AAW40351 (1-80)
 QY 16 ATGGCTAAGTTTGGTCCATCATCCGACCTCTTTTGTCTCTCTTGTCTTTTGTCTGCT 75
 Db 1 MetAlalysePheAlaSerIleIleAlaLeuPheAlaLeuValLeuPheAla 20
 QY 76 TTGGAAGCACCAATGCTGGAAGCACAGAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
 Db 21 PheAspAlaProAlaMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40

QY 136 TCAGAGTCTGTGGAACAATAACGATGCAAGATCAGTGCATTAAACCTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
QY 196 CGACATGGATCTTGCACACTATGCTTCCACGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80

RESULT 15

AAW40346

ID AAW40346 standard; protein; 80 AA.

XX

AC AAW40346;

XX

DT 23-JUN-1998 (first entry)

XX

DE A. thaliana PDF1.2 protein.

XX

KW Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;

KW fungi.

XX

OS Arabidopsis thaliana.

XX

XX

PH Key Location/Qualifiers

FT Peptide 1..29

FT Protein /label= signal

FT /label= PFD1.2

FT /note= "plant defensin"

XX

PN WO9800023-A2.

XX

PD 08-JAN-1998.

XX

PF 20-JUN-1997; 97WO-GB001672.

XX

PR 01-JUL-1996; 96GB-00013753.

XX

PA (ZENE) ZENECA LTD.

XX

PI Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras FRG, Manners JM;

PI Kazan K;

XX

DR WPI; 1998-086663/08.

XX

DR N-PSDB; AAV10633.

XX

PT Protecting plants against pathogens by inducing defensin genes - by

PT stimulating ethylene or jasmonate pathways, also new promoter of defensin

PT gene from Arabidopsis.

XX

PS Disclosure; Fig 1; 72pp; English.

XX

CC This sequence represents the Arabidopsis PDF1.2 protein which is used in

CC a novel method for the protection of plants against pathogens which

CC involves inducing expression of a plant defensin gene by stimulating the

CC jasmonate and/or ethylene pathways. The method is used to induce

CC protection against necrotrophic pathogens, specifically fungi and does

CC not require cytotoxic or potentially harmful chemicals

XX

SQ Sequence 80 AA;

Alignment Scores:

Pred. No.: 8.26e-36 Length: 80

Score: 403.00 Matches: 71

Percent Similarity: 95.00% Conservative: 5

Best Local Similarity: 88.75% Mismatches: 4

Query Match: 53.59% Indels: 0

DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x AAW40346 (1-80)

Db 1 MetalAlaLysPheAlaSerIleIleThrLeuIlePheAlaAlaLeuValLeuPheAlaAla 20
QY 76 TTCGNAAGCACCAACAATGGTGGGAAGCACAGAAGTTGTGCGAAAGGCCCAAGTGGGACATGG 135
Db 21 PheAspAlaProAlaMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTGGAACAATAACGATGCAAGATTCAGTGCATTAAACCTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
QY 196 CGACATGGATCTTGCACACTATGCTTCCACGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80

Search completed: May 11, 2004, 17:02:15
Job time : 62.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: May 11, 2004, 17:00:09 ; Search time 22 Seconds
(without alignments)
1943.014 Million cell updates/sec

Title: US-10-006-252A-19

Perfect score: 752

Sequence: 1 gttttattagatcatggc.....caaaaaaaaaaaaaaaaaaaaa 414

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778928

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10006252.cgn_1_27@runat_11052004_141658_22839 -NCPU=6 -ICFU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA.*
1: /cgn2_6/prodata/2/iaa/5A COMB.pcp.*
2: /cgn2_6/prodata/2/iaa/55 COMB.pcp.*
3: /cgn2_6/prodata/2/iaa/6A COMB.pcp.*
4: /cgn2_6/prodata/2/iaa/6B COMB.pcp.*
5: /cgn2_6/prodata/2/iaa/6CTUS COMB.pcp.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	442	58.8	80	1	US-08-377-687-49
2	442	58.8	80	2	US-08-777-192-49
3	442	58.8	80	3	US-08-971-982-49
4	434	57.7	80	3	US-09-103-489-20
5	434	57.7	80	4	US-09-829-381D-20
6	433	57.6	80	1	US-08-377-687-59
7	433	57.6	80	2	US-08-777-192-59
8	433	57.6	80	3	US-08-971-982-59
9	417	55.5	80	4	US-09-589-733C-21
10	397	52.8	80	4	US-09-589-733C-23
11	396.5	52.7	79	1	US-08-627-706-15
12	396.5	52.7	79	3	US-09-103-489-15

13	396.5	52.7	79	4	US-09-829-381D-15
14	309	41.1	51	1	US-08-377-687-19
15	309	41.1	51	1	US-08-627-706-18
16	309	41.1	51	2	US-08-777-192-19
17	309	41.1	51	3	US-08-971-982-19
18	309	41.1	51	3	US-09-103-489-18
19	309	41.1	51	4	US-09-077-951-8
20	309	41.1	51	4	US-09-077-948A-34
21	309	41.1	51	4	US-09-829-381D-18
22	309	41.1	51	4	US-09-589-733C-22
23	307	40.8	51	1	US-08-656-318A-3
24	307	40.8	51	2	US-08-956-459-3
25	302	40.2	51	4	US-09-077-951-58
26	302	40.2	51	4	US-09-077-951-60
27	301	40.0	51	4	US-09-077-951-57
28	300	39.9	51	1	US-08-627-706-19
29	300	39.9	51	3	US-09-103-489-19
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31	300	39.9	51	4	US-09-077-951-20
32	300	39.9	51	4	US-09-077-951-61
33	300	39.9	51	4	US-09-077-948A-35
34	300	39.9	51	4	US-09-829-381D-19
35	298	39.6	51	1	US-08-656-318A-4
36	298	39.6	51	2	US-08-956-459-4
37	296	39.4	51	4	US-09-077-951-22
38	296	39.4	51	4	US-09-077-951-29
39	296	39.4	51	4	US-09-077-951-65
40	295	39.2	51	4	US-09-077-951-31
41	295	39.2	51	4	US-09-077-951-39
42	295	39.2	51	4	US-09-077-951-44
43	295	39.2	51	4	US-09-077-951-77
44	294	39.1	51	4	US-09-077-951-28
45	294	39.1	51	4	US-09-077-951-41

ALIGNMENTS

RESULT 1

US-08-377-687-49
; Sequence 49, Application US/08377687
; Patent No. 538525
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEIDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCES/DOCKET NUMBER: 95042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-377-687-49

Alignment Scores:
Pred. No.: 5,13e-45 Length: 80
Score: 442.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 58.78% Indels: 0
DB: 1 Gaps: 0

US-10-006-252a-19 (1-414) x US-08-377-687-49 (1-80)

Qy 16 ATGGCTAAGTTTGGCTCCATCGCACTTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 MetAlaLysPheAlaSerIlelleAlaLeuPheAlaLeuValLeuPheAla 20
Qy 76 TTCGAGCACCACAACTGGTGGAGCACAGAGTTGTGGAAAGGCCAAGTGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
Qy 136 TCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATTAACTTGAAGAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Qy 196 CGACATGGATCTTGAACATGTCTTCCAGCTCACAAGTGTATCTGCTACTTCTGCTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 2

US-08-777-192-49

Sequence 49, Application US/08777192

Patent No. 5824869

GENERAL INFORMATION:

APPLICANT: BROEKERT, WILLEM F.

APPLICANT: CAMMUE, BRUNO P.A.

APPLICANT: OSBORN, RUPERT W.

APPLICANT: REES, SARAH B.

APPLICANT: TERRAS, FRANKY R.G.

APPLICANT: VANDERLEYDEN, JOZEF

TITLE OF INVENTION: BIOCIDAL PROTEINS

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN

STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/777,192

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/002,480

FILING DATE: 04-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3000

TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 80 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-777-192-49

Alignment Scores:
Pred. No.: 5,13e-45 Length: 80
Score: 442.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 58.78% Indels: 0
DB: 2 Gaps: 0

US-10-006-252a-19 (1-414) x US-08-777-192-49 (1-80)

Qy 16 ATGGCTAAGTTTGGCTCCATCGCACTTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 MetAlaLysPheAlaSerIlelleAlaLeuPheAlaLeuValLeuPheAla 20
Qy 76 TTCGAGCACCACAACTGGTGGAGCACAGAGTTGTGGAAAGGCCAAGTGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
Qy 136 TCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATTAACTTGAAGAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
Qy 196 CGACATGGATCTTGAACATGTCTTCCAGCTCACAAGTGTATCTGCTACTTCTGCTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 3

US-08-971-982-49

Sequence 49, Application US/08971982

Patent No. 6187904

GENERAL INFORMATION:

APPLICANT: BROEKERT, WILLEM F.

APPLICANT: CAMMUE, BRUNO P.A.

APPLICANT: OSBORN, RUPERT W.

APPLICANT: REES, SARAH B.

APPLICANT: TERRAS, FRANKY R.G.

APPLICANT: VANDERLEYDEN, JOZEF

TITLE OF INVENTION: BIOCIDAL PROTEINS

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN

STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/971,982

FILING DATE: 17-No. 6187904-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/002,480

FILING DATE: 04-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

QY 76 TTCGAGCACCACCAATGGTGGAGCAGACAGATTTGTGCGAAGGCCAAGTGGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTGGAACAATAAGCGCATGCAAGATCAGTGCATTAACTTGAAGAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
QY 196 CGACATGATCTTCCAACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 8

US-08-971-982-59

; Sequence 59, Application US/08971982

; Patent No. 6187904

; GENERAL INFORMATION:

; APPLICANT: BROEKAERT, WILLEM F.

; CAMMUE, BRUNO P. A.

; OSBORN, RUPERT W.

; REES, SARAH B.

; TERRAS, FRANKY R. G.

; VANDERLEIDEN, JOZEF

; TITLE OF INVENTION: BIOCIDAL PROTEINS

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARB & CUSHMAN

; STREET: 1100 NEW YORK AVENUE, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/971,982

; FILING DATE: 17-No. 6187904-1997

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/002,480

; FILING DATE: 04-JAN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: KOKULIS, PAUL N.

; REGISTRATION NUMBER: 16,773

; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3000

; TELEFAX: 202-822-0944

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 80 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 59:

US-08-971-982-59

Alignment Scores:

Pred. No.:	6,25e-44	Length:	80
Score:	433.00	Matches:	78
Percent Similarity:	98.75%	Conservative:	1
Best Local Similarity:	97.50%	Mismatches:	0
Query Match:	57.58%	Indels:	0
DB:	3	Gaps:	0

US-10-006-252A-19 (1-414) x US-08-971-982-59 (1-80)

QY 16 ATGGCTAAGTTGGTCCCATCATCGCACTTCTTTTGTGCTGCTTGTCTTTTGTGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20

QY 76 TTCGAGCACCACCAATGGTGGAGCAGACAGATTTGTGCGAAGGCCAAGTGGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTGGAACAATAAGCGCATGCAAGATCAGTGCATTAACTTGAAGAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
QY 196 CGACATGATCTTCCAACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 9

US-09-589-733C-21

; Sequence 21, Application US/09589733C

; Patent No. 6677503

; GENERAL INFORMATION:

; APPLICANT: Bidney, Dennis L.

; APPLICANT: Crasta, Oswald R.

; APPLICANT: Duwick, Jon

; APPLICANT: Hu, Xu

; APPLICANT: Lu, Guihua

; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and

; TITLE OF INVENTION: Genes and their Uses

; FILE REFERENCE: 5718-90

; CURRENT APPLICATION NUMBER: US/09/589,733C

; PRIOR FILING DATE: 2000-06-08

; PRIOR APPLICATION NUMBER: 60/140,646

; PRIOR FILING DATE: 1999-06-23

; PRIOR APPLICATION NUMBER: 60/162,904

; PRIOR FILING DATE: 1999-11-01

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 21

; LENGTH: 80

; TYPE: PRT

; ORGANISM: Raphanus sativus

US-09-589-733C-21

Alignment Scores:

Pred. No.:	5,32e-42	Length:	80
Score:	417.00	Matches:	74
Percent Similarity:	95.00%	Conservative:	2
Best Local Similarity:	92.50%	Mismatches:	4
Query Match:	55.45%	Indels:	0
DB:	4	Gaps:	0

US-10-006-252A-19 (1-414) x US-09-589-733C-21 (1-80)

QY 16 ATGGCTAAGTTGGTCCCATCATCGCACTTCTTTTGTGCTGCTTGTCTTTTGTGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleIleValLeuLeuPheValAlaLeuValPheAlaAla 20
QY 76 TTCGAGCACCACCAATGGTGGAGCAGACAGATTTGTGCGAAGGCCAAGTGGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTGGAACAATAAGCGCATGCAAGATCAGTGCATTAACTTGAAGAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
QY 196 CGACATGATCTTCCAACTATGTCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 10

US-09-589-733C-23

; Sequence 23, Application US/09589733C

; Patent No. 6677503

; GENERAL INFORMATION:

; APPLICANT: Bidney, Dennis L.

; APPLICANT: Crasta, Oswald R.

```
; APPLICANT: Duwick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; FILE REFERENCE: Genes and their Uses
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/09/589,733C
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-589-733C-23

Alignment Scores:
Pred. No.: 1,38e-39 Length: 90
Score: 397.00 Matches: 70
Percent Similarity: 92.50% Conservative: 4
Best Local Similarity: 87.50% Mismatches: 6
Query Match: 52.79% Indels: 0
DB: Gaps: 0

US-10-006-252A-19 (1-414) x US-09-589-733C-23 (1-80)
QY 16 ATGGCTAAAGTTGGCTGCATCATGCACTTCTTTTCTGCTCTCTGTTCTTTTCTGCT 75
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QY 76 TTCGAAGCACCACCAATGGTGGAGGACACAGAGTGTGGAAAGGCCAAGTGGGACATGG 135
Db 21 LeuGluAlaProMetValValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
QY 136 TCAGGAGCTGTGGAAACAATAACGATGCAAGATCAGTGCATTAACTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysLysLeuGluLysAla 60
QY 196 CGACATGATCTTGCATATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTCTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 11
US-08-627-706-15
; Sequence 15, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; NAME: Cohen, Charles E.

; APPLICANT: Duwick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; FILE REFERENCE: Genes and their Uses
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/09/589,733C
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-589-733C-23

Alignment Scores:
Pred. No.: 1,38e-39 Length: 90
Score: 397.00 Matches: 70
Percent Similarity: 92.50% Conservative: 4
Best Local Similarity: 87.50% Mismatches: 6
Query Match: 52.79% Indels: 0
DB: Gaps: 0

US-10-006-252A-19 (1-414) x US-09-589-733C-23 (1-80)
QY 16 ATGGCTAAAGTTGGCTGCATCATGCACTTCTTTTCTGCTCTCTGTTCTTTTCTGCT 75
Db 1 MetAlaLysSerAlaThrIleValThrLeuPheAlaAlaLeuValPheAlaAla 20
QY 76 TTCGAAGCACCACCAATGGTGGAGGACACAGAGTGTGGAAAGGCCAAGTGGGACATGG 135
Db 21 LeuGluAlaProMetValValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
QY 136 TCAGGAGCTGTGGAAACAATAACGATGCAAGATCAGTGCATTAACTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysLysLeuGluLysAla 60
QY 196 CGACATGATCTTGCATATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTCTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 12
US-09-103-489-15
; Sequence 15, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: US/09/103,489
; FILING DATE:
; NAME: Cohen, Charles E.
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REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-103-489-15

Alignment Scores:
Pred. No.: 1,58e-39
Score: 396.50
Percent Similarity: 96.25%
Best Local Similarity: 88.75%
Query Match: 52.73%
DB: 3
Gaps: 1

US-10-006-252A-19 (1-414) x US-09-103-489-15 (1-79)

QY 16 ATGGCTAAGTTGGTCCATCATCGCACTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 MetAlaLysPheAlaThrIleSerLeuLeuPheAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAAGCACCACAAATGGTGGAGACACAGAAGTTGTGCGAAAGGCCAAGTGGACATGG 135
Db 21 PheGluAlaProThrMetValAspAla---ArgLeuCysGluArgProSerGlyThrTrp 39
QY 136 TCAGAGCTCTGTGGAACATACGATGCAAGATCAGTGCATTAACTTGGAAAGCA 195
Db 40 SerGlyValCysGlyAsnAsnAlaCysArgAsnGlnCysArgAsnLeuGluArgAla 59
QY 196 CGACATGATCTTGCACACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
Db 60 GluHisGlySerCysAsnTyrrValPheProAlaHisCysileCysyrPheProCys 79

RESULT 13

US-09-829-381D-15
Sequence 15, Application US/09829381D
Patent No. 6653280
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shan, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFF from Alyssum and Methods for Control
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patent in version 3.1
SEQ ID NO 15
LENGTH: 79
TYPE: PRT
ORGANISM: Alyssum Sp.
US-09-829-381D-15

Alignment Scores:
Pred. No.: 1,58e-39
Score: 396.50
Percent Similarity: 96.25%
Best Local Similarity: 88.75%
Query Match: 52.73%
DB: 4
Gaps: 1

US-10-006-252A-19 (1-414) x US-09-829-381D-15 (1-79)

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QY 76 TTCGAAGCACCACAAATGGTGGAGACACAGAAGTTGTGCGAAAGGCCAAGTGGACATGG 135
Db 21 PheGluAlaProThrMetValAspAla---ArgLeuCysGluArgProSerGlyThrTrp 39
QY 136 TCAGAGCTCTGTGGAACATACGATGCAAGATCAGTGCATTAACTTGGAAAGCA 195
Db 40 SerGlyValCysGlyAsnAsnAlaCysArgAsnGlnCysArgAsnLeuGluArgAla 59
QY 196 CGACATGATCTTGCACACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
Db 60 GluHisGlySerCysAsnTyrrValPheProAlaHisCysileCysyrPheProCys 79

RESULT 14

US-08-377-687-19
Sequence 19, Application US/08377687
Patent No. 5538525
GENERAL INFORMATION:
APPLICANT: BROEKERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-377-687-19

Alignment Scores:
Pred. No.: 4,96e-29
Score: 309.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 41.09%
DB: 1
Gaps: 0

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Db 21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyrValPhe 40
QY 223 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
Db 41 ProAlaHisLysCysIleCysTyrPheProCys 51

RESULT 15

US-08-627-706-18
; Sequence 1B, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, B44F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-627-706-18

Alignment Scores:
Pred. No.: 4,96e-29 Length: 51
Score: 309.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.09% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-19 (1-414) x US-08-627-706-18 (1-51)

QY 103 CAGAAGTTGCGAAGCCCAAGTGGACATGTCAGAGTCTGTGGAACATAACGCA 162
Db 1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
QY 163 TGCAGAATCAGTCAGTCAATTAACCTTGAGAAACGACATGGATCTTGCAACTATGTCTTC 222

Db 21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyrValPhe 40
QY 223 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
Db 41 ProAlaHisLysCysIleCysTyrPheProCys 51

Search completed: May 11, 2004, 17:06:19
Job time : 27 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: May 11, 2004, 17:02:19 ; Search time 41.5 Seconds
(without alignments)
5537.958 Million cell updates/sec

Title: US-10-006-252A-19
Perfect score: 752
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Xgapop 10.0 , Ygapext 0.5
Xgapop 6.0 , Ygapext 7.0
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Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 2281346

Minimum DB seq length: 0

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Maximum Match 100%

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Database : Published Applications AA:

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- 6: /cgn2_6/ptodata/2/pubpaa/PTUS_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

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2	434	57.7	80	9	US-09-829-381A-20	Sequence 20, Appl
3	434	57.7	80	12	US-10-681-972-20	Sequence 20, Appl
4	433	57.6	80	9	US-09-759-584-59	Sequence 59, Appl
5	417	55.5	80	12	US-10-636-396-21	Sequence 21, Appl
6	403	53.6	80	9	US-09-732-561-16	Sequence 16, Appl
7	403	53.6	80	9	US-09-732-561-22	Sequence 22, Appl
8	397	52.8	80	9	US-09-732-561-14	Sequence 14, Appl
9	397	52.8	80	12	US-10-636-396-23	Sequence 23, Appl
10	396.5	52.7	79	9	US-09-829-381A-15	Sequence 15, Appl
11	396.5	52.7	79	12	US-10-681-972-15	Sequence 15, Appl
12	309	41.1	51	9	US-09-759-584-19	Sequence 19, Appl
13	309	41.1	51	9	US-09-732-561-19	Sequence 19, Appl
14	309	41.1	51	9	US-09-829-381A-18	Sequence 18, Appl
15	309	41.1	51	12	US-10-681-972-18	Sequence 18, Appl
16	309	41.1	51	12	US-10-388-361A-34	Sequence 34, Appl
17	309	41.1	51	12	US-10-636-396-22	Sequence 22, Appl
18	309	41.1	51	13	US-10-006-252A-8	Sequence 8, Appl
19	309	41.1	51	15	US-10-072-809A-33	Sequence 33, Appl
20	309	41.1	51	15	US-10-072-809A-35	Sequence 35, Appl
21	304	40.4	51	9	US-09-732-561-17	Sequence 17, Appl
22	303	40.3	51	15	US-10-072-809A-31	Sequence 31, Appl
23	302	40.2	51	13	US-10-006-252A-58	Sequence 58, Appl
24	302	40.2	51	13	US-10-006-252A-60	Sequence 60, Appl
25	301	40.0	51	13	US-10-006-252A-57	Sequence 57, Appl
26	300	39.9	51	9	US-09-829-381A-19	Sequence 19, Appl
27	300	39.9	51	12	US-10-681-972-19	Sequence 19, Appl
28	300	39.9	51	12	US-10-388-361A-35	Sequence 35, Appl
29	300	39.9	51	13	US-10-006-252A-20	Sequence 20, Appl
30	300	39.9	51	13	US-10-006-252A-61	Sequence 61, Appl
31	300	39.9	51	15	US-10-072-809A-31	Sequence 31, Appl
32	296	39.4	51	13	US-10-006-252A-22	Sequence 22, Appl
33	296	39.4	51	13	US-10-006-252A-29	Sequence 29, Appl
34	296	39.4	51	13	US-10-006-252A-65	Sequence 65, Appl
35	296	39.4	51	13	US-10-006-252A-31	Sequence 31, Appl
36	295	39.2	51	13	US-10-006-252A-39	Sequence 39, Appl
37	295	39.2	51	13	US-10-006-252A-44	Sequence 44, Appl
38	295	39.2	51	13	US-10-006-252A-77	Sequence 77, Appl
39	295	39.2	51	13	US-10-006-252A-28	Sequence 28, Appl
40	294	39.1	51	13	US-10-006-252A-41	Sequence 41, Appl
41	294	39.1	51	13	US-10-006-252A-42	Sequence 42, Appl
42	294	39.1	51	13	US-10-006-252A-59	Sequence 59, Appl
43	294	39.1	51	13	US-10-006-252A-23	Sequence 23, Appl
44	293	39.0	51	13	US-10-006-252A-26	Sequence 26, Appl
45	293	39.0	51	13	US-10-006-252A-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-759-584-49
; Sequence 49, Application US/09759584
; Patent No. US20010014732A1
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSEBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

[REDACTED]

ORGANISM: Raphanus sativus
US-10-681-972-20

Alignment Scores:
Pred. No.: 6,28e-41 Length: 80
Score: 434.00 Matches: 79
Percent Similarity: 98.75% Conservative: 0
Best Local Similarity: 98.75% Mismatches: 1
Query Match: 57.71% Indels: 0
DB: 12 Gaps: 0

US-10-006-252A-19 (1-414) x US-10-681-972-20 (1-80)

QY 16 ATGGCTAAGTTGGTCCATCATCGACCTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAAGCACCAACAATGGTGGAGCACAGATTGTGGAAAGGCCAAGTGGACATGG 135
Db 21 PheGluAlaGluThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
QY 136 TCAGAGTCTGTGGAACAATAACGCAATCAAGTGCATTAACCTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluLysAla 60
QY 196 CGACATGGATCTTGCACACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 4

US-09-759-584-59
Sequence 59, Application US/09759584
Patent No. US20010014732A1

GENERAL INFORMATION:
APPLICANT: BROEKERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-759-584-59

Alignment Scores:
Pred. No.: 8,18e-41 Length: 80
Score: 433.00 Matches: 78
Percent Similarity: 98.75% Conservative: 1
Best Local Similarity: 97.50% Mismatches: 1
Query Match: 57.58% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-19 (1-414) x US-09-759-584-59 (1-80)

QY 16 ATGGCTAAGTTGGTCCATCATCGACCTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheAlaAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAAGCACCAACAATGGTGGAGCACAGATTGTGGAAAGGCCAAGTGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
QY 136 TCAGAGTCTGTGGAACAATAACGCAATCAAGTGCATTAACCTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
QY 196 CGACATGGATCTTGCACACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 5

US-10-636-396-21
Sequence 21, Application US/10636396
Publication No. US20040073971A1

GENERAL INFORMATION:
APPLICANT: BIDNEY, DENNIS L.
APPLICANT: CRASTA, OSWALD R.
APPLICANT: DUVICK, JON
APPLICANT: HU, XU
APPLICANT: LU, GUIHUA
TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and Genes and their Uses
FILE REFERENCE: 5718-90
CURRENT APPLICATION NUMBER: US/10/636,396
CURRENT FILING DATE: 2003-08-07
PRIOR APPLICATION NUMBER: US/09/589,733C
PRIOR FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: 60/140,646
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/162,904
PRIOR FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21
LENGTH: 80
TYPE: PRT
ORGANISM: Raphanus sativus
US-10-636-396-21

Alignment Scores:
Pred. No.: 5,62e-39 Length: 80
Score: 417.00 Matches: 74
Percent Similarity: 95.00% Conservative: 2
Best Local Similarity: 92.50% Mismatches: 4
Query Match: 55.45% Indels: 0
DB: 12 Gaps: 0

US-10-006-252A-19 (1-414) x US-10-636-396-21 (1-80)

QY 16 ATGGCTAAGTTGGTCCATCATCGACCTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleAlaLeuLeuPheValAlaLeuValPheAlaAla 20
QY 76 TTCGAAGCACCAACAATGGTGGAGCACAGATTGTGGAAAGGCCAAGTGGACATGG 135

Db 21 PheGluGluProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40
 Qy 136 TCAGGAGTCTGGGAACAATAACCATGCAAGAAATCAGTGCATTAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluAla 60
 Qy 196 CGACATGGATCTTGCACACTATGCTCTCCAGCTCACAAAGTGTATCTGCTACTTCTCTTCT 255
 Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 6

US-09-732-561-16
 ; Sequence 16, Application US/09732561
 ; Patent No. US20020035738A1

GENERAL INFORMATION:

APPLICANT: Thoma, Bart
 APPLICANT: Terras, Franky
 APPLICANT: Penninckx, Iris
 APPLICANT: Manners, John
 APPLICANT: Broekaert, Willem
 TITLE OF INVENTION: Plant Protection Method
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZENECA AG Products
 STREET: 1800 Concord Pike
 CITY: Wilmington
 STATE: DE
 COUNTRY: USA
 ZIP: 19850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/732,561
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/202,638
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB97/01672
 FILING DATE: 20-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hohenschutz, Liza D.
 REGISTRATION NUMBER: 33,712
 REFERENCE/DOCKET NUMBER: PPD 50165/UST
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (302) 886-1699
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 80 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 STRAIN: PDF 1.2

Alignment Scores:

Pred. No.: 2,28e-37 Length: 80
 Score: 403.00 Matches: 71
 Percent Similarity: 95.00% Conservative: 5
 Best Local Similarity: 88.75% Mismatches: 4
 Query Match: 53.59% Indels: 0
 DB: 9 Gaps: 0

US-10-006-252A-19 (1-414) x US-09-732-561-16 (1-80)

Qy 16 ATGGCTAGTCTGGCCATCGCAGCTCTCTTTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 75
 Db 1 MetAlaLysPheAlaSerIleIleThrLeuIlePheAlaLeuValLeuPheAlaAla 20
 Qy 76 TTCGAGGACCAACCAATCGTGGAAAGCACAGAAGTTGTGCGAAAGCCCAAGTGGGACATGG 135
 Db 21 PheAspAlaProAlaMetValGluAlaGlnLysLeuCysGlnLysProSerGlyThrTrp 40
 Qy 136 TCAGGAGTCTGGGAACAATAACCATGCAAGAAATCAGTGCATTAACCTTGAGAAAGCA 195
 Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluAla 60
 Qy 196 CGACATGGATCTTGCACACTATGCTCTCCAGCTCACAAAGTGTATCTGCTACTTCTCTTCT 255
 Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80

RESULT 7

US-09-732-561-22
 ; Sequence 22, Application US/09732561
 ; Patent No. US20020035738A1

GENERAL INFORMATION:

APPLICANT: Thoma, Bart
 APPLICANT: Terras, Franky
 APPLICANT: Penninckx, Iris
 APPLICANT: Manners, John
 APPLICANT: Broekaert, Willem
 TITLE OF INVENTION: Plant Protection Method
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZENECA AG Products
 STREET: 1800 Concord Pike
 CITY: Wilmington
 STATE: DE
 COUNTRY: USA
 ZIP: 19850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/732,561
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/202,638
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB97/01672
 FILING DATE: 20-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hohenschutz, Liza D.
 REGISTRATION NUMBER: 33,712
 REFERENCE/DOCKET NUMBER: PPD 50165/UST
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (302) 886-1699
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 80 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 STRAIN: Arabidopsis PDF1.2 amino acid sequence

Alignment Scores:

Pred. No.: 2,28e-37 Length: 80
 Score: 403.00 Matches: 71
 Percent Similarity: 95.00% Conservative: 5
 Best Local Similarity: 88.75% Mismatches: 4

Query Match: 53.59% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-19 (1-414) x US-09-732-561-22 (1-80)

QY 16 ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTGCTCTTGTCTTTTGGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleThrLeuPheAlaAlaLeuValLeuPheAlaAla 20

QY 76 TTCGAAGCACCAACAATGGTGGAAAGCAGAGTGTGGAAAGGCCAAGTGGGACATCG 135
Db 21 PheAspAlaProAlaMetValGluAlaGlnLysLeuCysGlnLysProSerGlyThrTrp 40

QY 136 TCAGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATTAACTTGGAGAAGCA 195
Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGlnGlyAla 60

QY 196 CGACATGGATCTTCCAACTATGCTTCCAGCTCACAAGTGATCTGCTACTTCTCTTGT 255
Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80

RESULT 8

US-09-732-561-14

; Sequence 14, Application US/09732561

; Patent No. US20020035738A1

; GENERAL INFORMATION:

; APPLICANT: Thoma, Bart

; APPLICANT: Terras, Franky

; APPLICANT: Penninx, Iris

; APPLICANT: Manners, John

; APPLICANT: Kazan, Kemal

; APPLICANT: Broekaert, Willem

; TITLE OF INVENTION: Plant Protection Method

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ZENECA Ag Products

; STREET: 1800 Concord Pike

; CITY: Wilmington

; STATE: DE

; COUNTRY: USA

; ZIP: 19850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/732,561

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/202,638

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB97/01672

; FILING DATE: 20-JUN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Hohenschutz, Liza D.

; REGISTRATION NUMBER: 33,712

; REFERENCE/DOCKET NUMBER: PPD 50165/UST

; TELEPHONE: (302) 886-1699

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 80 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; STRAIN: PDF1.1

US-09-732-561-14

Alignment Scores:

Pred. No.: 1.11e-36 Length: 80

Score: 397.00 Matches: 70

Percent Similarity: 92.50% Conservative: 4

Best Local Similarity: 87.50% Mismatches: 6

Query Match: 52.79% Indels: 0

DB: 9 Gaps: 0

US-10-006-252A-19 (1-414) x US-09-732-561-14 (1-80)

QY 16 ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTGCTCTTGTCTTTTGGCTGCT 75
Db 1 MetAlaLysSerAlaThrIleValThrLeuPheAlaAlaLeuValPheAlaAla 20

QY 76 TTCGAAGCACCAACAATGGTGGAAAGCAGAGTGTGGAAAGGCCAAGTGGGACATGG 135
Db 21 LeuGluAlaProMetValValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40

QY 136 TCAGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATTAACTTGGAGAAGCA 195
Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGlnGlyAla 60

QY 196 CGACATGGATCTTCCAACTATGCTTCCAGCTCACAAGTGATCTGCTACTTCTCTTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 9

US-10-636-396-23

; Sequence 23, Application US/10636396

; Publication No. US20040073971A1

; GENERAL INFORMATION:

; APPLICANT: Bidney, Dennis L.

; APPLICANT: Crasta, Oswald R.

; APPLICANT: Davick, Jon

; APPLICANT: Hu, Xu

; APPLICANT: Lu, Guihua

; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and

; TITLE OF INVENTION: Genes and their Uses

; FILE REFERENCE: 5718-90

; CURRENT APPLICATION NUMBER: US/10/636,396

; CURRENT FILING DATE: 2003-08-07

; PRIOR APPLICATION NUMBER: US/09/589,733C

; PRIOR FILING DATE: 2000-06-08

; PRIOR APPLICATION NUMBER: 60/140,646

; PRIOR FILING DATE: 1999-06-23

; PRIOR APPLICATION NUMBER: 60/162,904

; PRIOR FILING DATE: 1999-11-01

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 23

; LENGTH: 80

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-10-636-396-23

Alignment Scores:

Pred. No.: 1.11e-36 Length: 80

Score: 397.00 Matches: 70

Percent Similarity: 92.50% Conservative: 4

Best Local Similarity: 87.50% Mismatches: 6

Query Match: 52.79% Indels: 0

DB: 12 Gaps: 0

US-10-006-252A-19 (1-414) x US-10-636-396-23 (1-80)

QY 16 ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTGCTCTTGTCTTTTGGCTGCT 75
Db 1 MetAlaLysSerAlaThrIleValThrLeuPheAlaAlaLeuValPheAlaAla 20

QY 76 TTCGAAGCACCAACAATGGTGGAAAGCAGAGTGTGGAAAGGCCAAGTGGGACATGG 135
Db 21 LeuGluAlaProMetValValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40

QY 136 TCAGGAGTCTGTGGAACAATACCATGCAAGATCAGTGCATTAACCTTGGAAGCA 195
Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysLeuAsnLeuGluLysAla 60
QY 196 CGACATGATCTTGCACAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255
Db 61 ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysileCysTyrPheProCys 80

RESULT 10

US-09-829-381A-15
; Sequence 15, Application US/09829381A
; Patent No. US20020144306A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jinhong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yannie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/829,381A
; APPLICATION NUMBER: US/09/829,381A
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-829-381A-15

Alignment Scores:
Pred. No.: 1.27e-36 Length: 79
Score: 396.50 Matches: 71
Percent Similarity: 96.25% Conservative: 6
Best Local Similarity: 88.75% Mismatches: 2
Query Match: 52.73% Indels: 1
DB: 9 Gaps: 1

US-10-006-252A-19 (1-414) x US-09-829-381A-15 (1-79)

QY 16 ATGGTAAGTTGGTGCATCATCGCACTTCTTTTGTGCTCTTTTGTCTTCTTCTGCT 75
Db 1 MetAlaLysPheAlaThrIleSerLeuPheAlaAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAAGCACCAACAATGTTGGAAGCACAGAGTTGCGAAGCCCAAGTGGGACATGG 135
Db 21 PheGluAlaProThrMetValAspAla--ArgLeuCysGluArgProSerGlyThrTrp 39

QY 136 TCAGGAGTCTGTGGAACAATACCATGCAAGATCAGTGCATTAACCTTGGAAGCA 195
Db 40 SerGlyValCysGlyAsnSerAsnAlaCysArgAsnGlnCysArgAsnLeuGluArgAla 59
QY 196 CGACATGATCTTGCACAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255
Db 60 GluHisGlySerCysAsnTyrValPheProAlaHisLysCysileCysTyrPheProCys 79

RESULT 11

US-10-681-972-15
; Sequence 15, Application US/10681972
; Publication No. US20040064850A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jinhong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yannie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
; TITLE OF INVENTION: Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/10/681,972
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 79
; TYPE: PPT
; ORGANISM: Alyssum Sp.
US-10-681-972-15

Alignment Scores:
Pred. No.: 1.27e-36 Length: 79
Score: 396.50 Matches: 71
Percent Similarity: 96.25% Conservative: 6
Best Local Similarity: 88.75% Mismatches: 2
Query Match: 52.73% Indels: 1
DB: 12 Gaps: 1

US-10-006-252A-19 (1-414) x US-10-681-972-15 (1-79)

QY 16 ATGGTAAGTTGGTGCATCATCGCACTTCTTTTGTGCTCTTTTGTCTTCTTCTGCT 75
Db 1 MetAlaLysPheAlaThrIleSerLeuPheAlaAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAAGCACCAACAATGTTGGAAGCACAGAGTTGCGAAGCCCAAGTGGGACATGG 135
Db 21 PheGluAlaProThrMetValAspAla--ArgLeuCysGluArgProSerGlyThrTrp 39
QY 136 TCAGGAGTCTGTGGAACAATACCATGCAAGATCAGTGCATTAACCTTGGAAGCA 195
Db 40 SerGlyValCysGlyAsnSerAsnAlaCysArgAsnGlnCysArgAsnLeuGluArgAla 59
QY 196 CGACATGATCTTGCACAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255
Db 60 GluHisGlySerCysAsnTyrValPheProAlaHisLysCysileCysTyrPheProCys 79

RESULT 12

US-09-759-584-19
; Sequence 19, Application US/09759584
; Patent No. US20010014732A1
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS

; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DABY & CUSHMAN
 ; STREET: 1100 NEW YORK AVENUE, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/759,584
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/377,687
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOKULIS, PAUL N.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-861-3000
 ; TELEFAX: 202-822-0944
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 51 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; CLONE: Rs-AFP1
 ; US-09-759-584-19

Alignment Scores:
 Pred. No.: 1.28e-26 Length: 51
 Score: 309.00 Matches: 51
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 41.09% Indels: 0
 DB: 9 Gaps: 0

US-10-006-252A-19 (1-414) x US-09-759-584-19 (1-51)

QY 103 CAGAGTTGTGCGAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACAATAACGCA 162
 Db 1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
 QY 163 TCGAAGATCAGTGCATTAACCTTGAGAAAGCACACATGATGTCGAACTATGCTTC 222
 Db 21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyrValPhe 40
 QY 223 CCAGCTCACAGTGTATCTGCTACTTCTTCTTGT 255
 Db 41 ProAlaHisLysCysIleCysTyrPheProCys 51

RESULT 13

; US-09-732-561-19
 ; Sequence 19, Application US/09732561
 ; Patent No. US20020035738A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thoma, Bart
 ; APPLICANT: Terras, Franky
 ; APPLICANT: Penninckx, Iris
 ; APPLICANT: Manners, John
 ; APPLICANT: Kazan, Kemal
 ; APPLICANT: Broekaert, Willem
 ; TITLE OF INVENTION: Plant Protection Method
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ZENECA Ag Products

; STREET: 1800 Concord Pike
 ; CITY: Wilmington
 ; STATE: DE
 ; COUNTRY: USA
 ; ZIP: 19850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/732,561
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/202,638
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB97/01672
 ; FILING DATE: 20-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hohenschulz, Liza D.
 ; REGISTRATION NUMBER: 33,712
 ; REFERENCE/DOCKET NUMBER: PPD 50165/UST
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (302) 886-1699
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 51 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; IMMEDIATE SOURCE:
 ; CLONE: Rs-AFP1
 ; US-09-732-561-19

Alignment Scores:
 Pred. No.: 1.28e-26 Length: 51
 Score: 309.00 Matches: 51
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 41.09% Indels: 0
 DB: 9 Gaps: 0

US-10-006-252A-19 (1-414) x US-09-732-561-19 (1-51)

QY 103 CAGAGTTGTGCGAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACAATAACGCA 162
 Db 1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
 QY 163 TCGAAGATCAGTGCATTAACCTTGAGAAAGCACACATGATGTCGAACTATGCTTC 222
 Db 21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyrValPhe 40
 QY 223 CCAGCTCACAGTGTATCTGCTACTTCTTCTTGT 255
 Db 41 ProAlaHisLysCysIleCysTyrPheProCys 51

RESULT 14

; US-09-829-381A-18
 ; Sequence 18, Application US/09829381A
 ; Patent No. US20020144306A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liang, Jihong
 ; APPLICANT: Shah, Dilip M.
 ; APPLICANT: Wu, Yonnie S.
 ; APPLICANT: Rosenberger, Cindy A.
 ; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
 ; Controlling Plant Pathogenic Fungi
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F

STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-829-381A-18

Alignment Scores:
Pred. No.: 1.28e-26 Length: 51
Score: 309.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.09% Indels: 0
DB: 9 Gaps: 0

US-10-006-252A-19 (1-414) x US-09-829-381A-18 (1-51)

Qy 103 CAGAAGTTGTGCGAAGCCGAAGTGGGACATGTCAGAGTCTGTGGAACAATAACGCA 162
Db 1 GlnLysLeuCysGluArgProSerGlyThrTripSerGlyValCysGlyAsnAsnAla 20
Qy 163 TGCAGACATCAGTCATTAACTTACAGAAAGCAGACATGATCTTGCACACTATGCTTTC 222
Db 21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyrValPhe 40
Qy 223 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
Db 41 ProAlaHisLysCysIleCysTy-PheProCys 51

RESULT 15

US-10-681-972-18
Sequence 18, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide AlyAPP from Alyseum and Methods for Control
TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489

PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 51
TYPE: PRT
ORGANISM: *Raphanus sativus*
US-10-681-972-18
Alignment Scores:
Pred. No.: 1.28e-26 Length: 51
Score: 309.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.09% Indels: 0
DB: 12 Gaps: 0
US-10-006-252A-19 (1-414) x US-10-681-972-18 (1-51)
Qy 103 CAGAAGTTGTGCGAAGCCGAAGTGGGACATGTCAGAGTCTGTGGAACAATAACGCA 162
Db 1 GlnLysLeuCysGluArgProSerGlyThrTripSerGlyValCysGlyAsnAsnAla 20
Qy 163 TGCAGACATCAGTCATTAACTTACAGAAAGCAGACATGATCTTGCACACTATGCTTTC 222
Db 21 CysLysAsnGlnCysIleAsnLeuGluLysAlaArgHisGlySerCysAsnTyrValPhe 40
Qy 223 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
Db 41 ProAlaHisLysCysIleCysTy-PheProCys 51
Search completed: May 11, 2004, 17:07:51
Job time : 42.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 11, 2004, 16:59:19 ; Search time 18.5 Seconds
(without alignments)
4305.221 Million cell updates/sec

Title: US-10-006-252A-19
Perfect score: 752
Sequence: 1 gttttattagtcattggc.....caaaaaaaaaaaaaaaaaa 414

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool_p/US10006252/runat.11052004.141658.22811/app.query.fasta.1.583
-DB=PIR_78 -QMT=fastan -SUFFIX=vr -MINMATCH=0.1 -LOPCU=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFM=ptc -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10006252 @CGN 1.1.38 @runat.11052004.141658.22811 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	442	58.8	80	T10176	antifungal protein
2	417	55.5	80	T10823	antifungal protein
3	405	53.9	80	T10183	antifungal protein
4	400	53.2	80	T02621	antifungal protein
5	399	53.1	80	T02622	probable antifunga
6	397	52.8	80	F96787	probable antifunga
7	394.5	52.5	79	T07917	protein T4O12.7 [i
8	393.5	52.3	79	T10243	antifungal protein
9	207	27.5	80	F96591	antifungal protein
10	175	23.3	30	S28991	probable antifunga
11	164	21.8	56	G83328	antifungal protein
12	161	21.4	27	S28989	hypothetical prote
13	156	20.7	27	S28995	antifungal protein
14	154	20.5	50	S66221	antifungal protein

15	151	20.1	25	2	S28993	antifungal protein
16	149	19.8	26	2	S28994	antifungal protein
17	149	19.8	161	2	S12246	antifer-specific pr
18	146.5	19.5	50	2	S66218	defensin AMP1 - Ae
19	145.5	19.3	49	2	S66219	defensin AMP1 - Cl
20	145.5	19.3	54	2	S66220	defensin AMP1 - He
21	142	18.9	27	2	S28990	antifungal protein
22	141.5	18.8	105	2	S57809	antifungal protein
23	115	15.3	83	2	T14866	gamma-thionin-like
24	114	15.2	105	2	S23574	probable gamma-thi
25	113	15.0	152	2	S46272	thionin precursor,
26	110.5	14.7	83	2	T03673	antifer-specific pr
27	99	13.2	73	2	D84333	piti protein (clon
28	95	12.6	75	2	S11156	proteinase inhibit
29	93.5	12.4	74	2	T06766	PSA10 protein - c
30	91.5	12.2	81	2	T02667	disease resistance
31	90.5	12.1	380	2	T04508	proteinase inhibit
32	87.5	11.6	72	2	T06599	hypothetical prote
33	83	11.0	77	2	C84333	disease resistance
34	82.5	11.1	221	2	T22771	proteinase inhibit
35	82	10.9	77	2	S30578	hypothetical prote
36	81.5	10.8	79	2	T06381	protease inhibitor
37	81	10.8	92	2	JC7897	proteinase inhibit
38	80	10.6	77	2	B84333	defensin 1 precurs
39	80	10.6	833	2	S19087	proteinase inhibit
40	79	10.5	77	2	T14395	gene Delta protein
41	79	10.5	768	2	I53821	proteinase inhibit
42	79	10.5	832	2	A31246	P-selectin - rat
43	79	10.5	880	2	S00670	neurogenic protein
44	77.5	10.3	467	2	S00839	neurogenic repetit
45	77	10.2	121	2	S17718	UTR2 protein - yea
						antifer-specific pr

ALIGNMENTS

RESULT 1

T10176
antifungal protein 1 precursor - radish
C:Species: Raphanus sativus (radish)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
C:Accession: T10176; A42842
R:Terras, P.R.; Eggermont, K.; Kovaleva, V.; Raikhel, N.V.; Osborn, R.W.; Kester, A.
Plant Cell 7, 568-573, 1995
A:Title: Small cysteine-rich antifungal proteins from radish: their role in host def.
A:Reference number: Z16976
A:Accession: T10176
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-80 <TER>
A:Cross-references: EMBL:U18557; NID:G644773; PID:G609322
A:Experimental source: strain ronde rode kleine witpunt; tissue type seed
R:Terras, P.R.; Schoofs, H.M.; De Bolle, M.F.; Van Deuven, F.; Rees, S.B.; Vanderley
J. Biol. Chem. 267, 15301-15309, 1992
A:Title: Analysis of two novel classes of plant antifungal proteins from radish (Rapi
A:Reference number: A42842; MUID:92348373; PMID:1639777
A:Accession: A42842
A>Status: preliminary
A:Molecule type: protein
A:Residues: 30-73 <TE2>
A:Experimental source: seed
A>Note: sequence extracted from NCBI backbone (NCBIP:109570)
C:Genetics:
A:Gene: APPI
C:Function:
A:Description: involved in creation of a microenvironment around the seed in which fi
A>Note: preferentially released during seed germination
C:Superfamily: gamma-thionin
C:Keywords: antifungal
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-80/Product: antifungal protein 1 #status predicted <MAT>

Alignment Scores: 1.8e-39 Length: 80
Pred. No.: 1.8e-39

US-10-006-252A-19 (1-414) x T10176 (1-80)

A:Cross-references: EMBL:X97318
 A:Experimental source: cultivar Ronde Kleine Witpunt
 C:Genetics:
 A:Gene: AFP4
 C:Superfamily: Gamma-thionin
 C:Keywords: antifungal
 F1-29/Domain: signal sequence #status predicted <SIG>
 F130-80/Product: antifungal protein 4 #status predicted <MAT>
 Alignment Scores:

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      4382833
Score: 405.00
Percent Similarity: 92.50%
Best Local Similarity: 90.00%
Query Match: 53.86%
DB: 2
US-10-006-252A-19 (1-414) x T10183 (1-50)
QY 16 ATGGCTAACTTTGGCTCCATCGACATCTTTTGGCTCTTGATCTTTTGGCT 75

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Db	1	Me	Ala	Ala	Ser	Val	Ser	Ile	Thr	Leu	Leu	Pro	Val	Ala	Leu	Val	Leu	Pro	Ala	20		
QY	76	TT	CG	AA	GC	CA	CA	CA	CA	AG	TGT	TC	GA	AG	CG	CA	AT	GG	CA	AT	GG	135
Db	21	Phe	Glu	Ala	Pro	Thr	Met	Val	Glu	Ala	Gln	Leu	Cys	Glu	Arg	Ser	Ser	Gly	Thr	Trp	40	

[illegible]

RESULT 4

T02621

probable antifungal protein T9918.17 - Arabidopsis thaliana

C.Species: Arabidopsis thaliana (mouse-ear cress)

C.Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001

C.Accession: T02621; 884655

R.ounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C. submitted to the EMBL Data Library, August 1998

A.Description: Randomlyps
 A.Reference number: Z14561
 A.Accession: T02621
 A.Status: translated from GE/EMBL/DDJ
 A.Molecule type: DNA
 A.Residues: 1-80 <ROU>

A;Cross-references: EMBL:AC004747; NID:g3413696; PID:g3413721
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84655
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-80 <STO>
A;Cross-references: GB:AE002093; NID:g3413721; PIDN:AAC31234.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g26020; T19L18.17
A;Map position: 2
A;Introns: 22/1
C;Superfamily: gamma-thionin

Alignment Scores:
Pred. No.: 6.32e-35 Length: 80
Score: 400.00 Matches: 70
Percent Similarity: 93.75% Conservative: 5
Best Local Similarity: 87.50% Mismatches: 5
Query Match: 53.19% Indels: 0
DB: 2 Gaps: 0

US-10-006-252a-19 (1-414) x T02621 (1-80)

QY 16 ATGGCTAAGTTGGTCCATCGCACCTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 MetAlalysPheAlaSerIleThrPheIleThrPheAlaLeuValPheAlaA 20

QY 76 TTCGAGCACCAACAATGTGGAGCACAGAGTGTGGCAAGCCAGTGGGACATGG 135
Db 21 PheGluValProThrMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40

QY 136 TCAGGAGTCTGTGGAACAATACGATCAGCAATCACTGCTACCTTGAAGAACA 195
Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60

QY 196 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGCTTCTTGT 255
Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 5
T02622
probable antifungal protein T19L18.18 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
C;Accession: T02622; D84655
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.
A;Reference number: Z14681
A;Accession: T02622
A;Status: translated from GB/EMBL/DBSJ
A;Molecule type: DNA
A;Residues: 1-80 <ROU>
A;Cross-references: EMBL:AC004747; NID:g3413696; PID:g3413711
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84655
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-80 <STO>
A;Cross-references: GB:AE002093; NID:g3413711; PIDN:AAC31234.1; GSPDB:GN00139
C;Genetics:

A;Gene: At2g26010; T19L18.18
A;Map position: 2
A;Introns: 22/1
C;Superfamily: gamma-thionin

Alignment Scores:
Pred. No.: 8.11e-35 Length: 80
Score: 399.00 Matches: 71
Percent Similarity: 93.75% Conservative: 4
Best Local Similarity: 88.75% Mismatches: 5
Query Match: 53.06% Indels: 0
DB: 2 Gaps: 0

US-10-006-252a-19 (1-414) x T02622 (1-80)

QY 16 ATGGCTAAGTTGGTCCATCGCACCTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 MetAlalysSerAlaAlaIleIleThrPheLeuPheAlaAlaLeuValPheAlaA 20

QY 76 TTCGAGCACCAACAATGTGGAGCACAGAGTGTGGCAAGCCAGTGGGACATGG 135
Db 21 PheGluAlaProIleMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40

QY 136 TCAGGAGTCTGTGGAACAATACGATCAGCAATCACTGCTACCTTGAAGAACA 195
Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60

QY 196 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGCTTCTTGT 255
Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 6
F96787
protein T4012.7 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Accession: F96787
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F96787
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-80 <STO>
A;Cross-references: GB:AE005173; NID:g6721100; PIDN:AAF26754.1; GSPDB:GN00141
C;Genetics:
A;Gene: T4012.7
A;Map position: 1
C;Superfamily: gamma-thionin

Alignment Scores:
Pred. No.: 1.33e-34 Length: 80
Score: 397.00 Matches: 70
Percent Similarity: 92.50% Conservative: 4
Best Local Similarity: 87.50% Mismatches: 6
Query Match: 52.79% Indels: 0
DB: 2 Gaps: 0

US-10-006-252a-19 (1-414) x F96787 (1-80)

QY 16 ATGGCTAAGTTGGTCCATCGCACCTCTTTTGGCTGCTCTTTTGGCTGCT 75
Db 1 MetAlalysSerAlaThrIleValThrPhePheAlaAlaLeuValPheAlaA 20

QY 76 TTCGAGCACCAACAATGTGGAGCACAGAGTGTGGCAAGCCAGTGGGACATGG 135

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Db      21  LeuGluAlaProMetValValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40
QY      136  TCAGGAGTCTGGGAACAATAACCATGCAAGAAATCAGTGCATTAACCTTGAGAAAGCA 195
Db      41  SerGlyValCysGlyAsnSerAsnAlaCysAsnGlnCysIleAsnLeuGluLysAla 60
QY      196  CGACATGGATCTTGAACATCTCTCCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
Db      61  ArgHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 7
T07917
antifungal protein - rape
C:Species: Brassica napus (rape)
C>Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jun-2000
C:Accession: T07917
R/Sohn, U.; Lee, C.M.; Lee, M.H.; Kim, J.H.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z16214
A:Accession: T07917
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-79 <SOH>
A:Cross-references: EMBL:U59459; NID:gl399229; PIDN:AB03224.1; PID:gl399230
A:Experimental source: cv. Naehan
C:Superfamily: gamma-thionin

Alignment Scores:
Pred. No.: 2,49e-34 Length: 79
Score: 394.50 Matches: 73
Percent Similarity: 93.75% Conservative: 2
Best Local Similarity: 91.25% Mismatches: 4
Query Match: 52.48% Indels: 1
DB: 2 Gaps: 1

US-10-006-252a-19 (1-414) x T07917 (1-79)

QY      16  ATGGCTAAGTTTGGCTCCATCATGCACTCTCTTTTGGCTCTCTTTTGGCTGT 75
Db      1  MetAlaLysPheAlaSerIleLeuLeuPheAlaLeuValPheAlaAla 20
QY      76  TTCGAAGCACCAATCGTGGAGACAGAGAGTTGTGCAAGGCCAAGTGGGACATGG 135
Db      21  PheGluAlaProThrMetValGluAla---LysLeuCysGluArgSerGlyThrTrp 39
QY      136  TCAGGAGTCTGGGAACAATAACCATGCAAGAAATCAGTGCATTAACCTTGAGAAAGCA 195
Db      40  SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleArgLeuGluGlyAla 59
QY      196  CGACATGGATCTTGAACATCTCTCCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
Db      60  GlnHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 79

RESULT 8
T10243
antifungal protein 3 precursor - radish
C:Species: Raphanus sativus (radish)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C:Accession: T10243
R/Terras, F.R.G.; Goderis, I.J.; Penninckx, I.J.; Osborn, R.W.; Broekaert, W.F.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z16994
A:Accession: T10243
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-79 <TER>
A:Cross-references: EMBL:X97319
A:Experimental source: cultivar Ronde Rode Kleine Witpunt
C:Genetics:
A:Gene: AFP3
C:Superfamily: gamma-thionin
C:Keywords: antifungal

```

F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-79/Product: antifungal protein 3 #status predicted <MAT>

Alignment Scores:
Pred. No.: 3.2e-34 Length: 79
Score: 393.50 Matches: 72
Percent Similarity: 95.00% Conservative: 4
Best Local Similarity: 90.00% Mismatches: 3
Query Match: 52.33% Indels: 1
DB: 2 Gaps: 1

US-10-006-252a-19 (1-414) x T10243 (1-79)

```

QY      16  ATGGCTAAGTTTGGCTCCATCATGCACTCTCTTTTGGCTCTCTTTTGGCTGT 75
Db      1  MetAlaLysPheAlaSerIleValAlaLeuPheAlaLeuValPheAlaAla 20
QY      76  TTCGAAGCACCAATCGTGGAGACAGAGAGTTGTGCAAGGCCAAGTGGGACATGG 135
Db      21  PheGluAlaProThrValValGluAla---LysLeuCysGluArgSerGlyThrTrp 39
QY      136  TCAGGAGTCTGGGAACAATAACCATGCAAGAAATCAGTGCATTAACCTTGAGAAAGCA 195
Db      40  SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleArgLeuGluGlyAla 59
QY      196  CGACATGGATCTTGAACATCTCTCCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
Db      60  GlnHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrPheProCys 79

```

RESULT 9

P96591
Probable antifungal protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C:Accession: F96591
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.-C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Mailli, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F96591
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-80 <STO>
A:Cross-references: GB:AE005173; NID:99857525; PIDN:AAG00880.1; GSPDB:GN00141
C:Genetics:
A:Gene: T24C10.12
A:Map position: 1
C:Superfamily: gamma-thionin

Alignment Scores:
Pred. No.: 4.93e-14 Length: 80
Score: 207.00 Matches: 40
Percent Similarity: 67.90% Conservative: 15
Best Local Similarity: 49.38% Mismatches: 24
Query Match: 27.53% Indels: 2
DB: 2 Gaps: 2

US-10-006-252a-19 (1-414) x F96591 (1-80)

```

QY      16  ATGGCTAAGTTTGGCTCCATCATGCACTCTCTTTTGGCTCTCTTTTGGCTGT 75
Db      1  MetAlaLysPheCysThrThrLeuLeuValAlaLeuValPheAlaAsp 20
QY      76  TTCGAGACCAACCAATCGTGGAGACAGAGAGTTGTGCAAGGCCAAGTGGGACATGG 135
Db      21  PheGluAlaProThrIleValLysAlaGlu---LeuLysArgGluSerGlyThrTrp 39

```

Alignment Scores:	
Pred. NO.:	2,31e-09
Score:	164.00
Length:	56
Matches:	25
Conservative:	7
Best Local Similarity:	50.00%
Mismatches:	18
Query Match:	21.81%
Indels:	0
Gaps:	0
DB:	2

Db	7	ArgIleCysGluAra-gserLysThrTrpThr-GlyPheCysGlyAsnThrArgGlyCys	26
QY	166	AAGAATCATGTCATTAAACCTTGAGAAAGCAGCATGGATCTTTGGCAACTATGCTTTCCCA	225
Db	27	AspSerGlnCysLysAra-gtrpGluAraGalaSerHisGlyAlaCysHisAlaGlnPhePro	46
QY	226	GCTCACAAAGTGTATCTGCTACTTTCCTTGT	255
Db	47	GlyPheAlaCysPheCysTyrPheAsnCys	56

RSS Lett. 31b, 233-240, 1993
 A.Protein: A new family of basic cysteine-rich plant antifungal proteins from Brassica
 A.Reference number: S28989; MUID:93138130; PMID:8422949
 A.Accession: S28989
 A.Molecule type: protein
 A.Residues: 1-27 <TER>
 C.Superfamily: gamma-thionin

Alignment Scores:	
Pred. No.:	5.24e-09
Length:	27
Score:	161.00
Matches:	27
Conservative:	0
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Mismatches:	0
Query Match:	21.41%
Indels:	0
DB:	2
Gaps:	0

DS:	Z	Gaps:	U
US-10-006-252A-19	(1-414) x S28989 (1-27)		
QY	103	CAGAAGTGTGCGAAGGCCAAGTCGGACATGCTCAGGAGCTCTGTGGAAACAATACGCA	162
Db	1	GlnLvsLeuCysGluAaGPrSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAla	20

[illegible]

RESULT 13
S28995
antifungal protein 1 - Arabidopsis thaliana (fragment)
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
C/Accession: S28995
R/Terras, F.R.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.
FEBS Lett. 316, 233-240, 1993
A/Title: A new family of basic cysteine-rich plant antifungal proteins from *Br...*
A/Reference number: S28999; MUID:93138130; PMID:8422949

A:Accession: S28995
 A:Molecule type: Protein
 A:Residues: 1-27 <TER>
 C:Superfamily: gamma-thionin

Alignment Scores:
 Pred. No.: 1.82e-08
 Length: 27

Score: 156.00 Matches: 26
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 96.30% Mismatches: 0
Query Match: 20.74% Indels: 0
DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x S28993 (1-27)

Qy 103 CAGAACTTGTGGAAAGCCCAAGTGGACATGGTCAGAGTCTGTGGAAACAATAACGCA 162
Db 1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnSerAsnAla 20
Qy 163 TGCAGAAATCAGTGCATTAAAC 183
Db 21 CysLysAsnGlnCysIleAsn 27

RESULT 14

S66221
Defensin AMP1 - Dahlia merckii
N:Alternate names: seed antifungal protein
C:Species: Dahlia merckii
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
C:Accession: S66221
R:Osborn, R.W.; de Samblanx, G.W.; Thevissen, K.; Goderis, I.; Torrekens, S.; van Leuven
FEBS Lett. 368, 257-262, 1995
A:Title: Isolation and characterisation of plant defensins from seeds of Asteraceae, Fab
A:Reference number: S66218; MUID:95354848; PMID:7628617
A:Molecule type: protein
A:Accession: S66221
A:Residues: 1-50 <OSB>
C:Keywords: antifungal

Alignment Scores:

Pred. No.: 2,82e-08 Length: 50
Score: 154.00 Matches: 26
Percent Similarity: 62.00% Conservative: 5
Best Local Similarity: 52.00% Mismatches: 19
Query Match: 20.48% Indels: 0
DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x S66221 (1-50)

Qy 106 AAGTTGTGGAAAGCCCAAGTGGACATGGTCAGAGTCTGTGGAAACAATAACGCAATGC 165
Db 1 GluLeuCysGluArgProSerGlyThrTrpSerGlyAsnGlyAsnThrGlyHisCys 20
Qy 166 AAGAATCAGTGCATTAAACCTTGAGAAAGCAGACATGGATCTTGCACACTATGCTTCCCA 225
Db 21 AspAsnGlnCysLysSerTrpGluGlyAlaAlaHisGlyAlaCysHisValArgAsnGly 40
Qy 226 GCTCACAAAGTGTATCTGCTACTTCTCTGT 255
Db 41 LysHisMetCysPheCysTyrPheAsnCys 50

RESULT 15

S28993
antifungal protein 1 - white mustard (fragment)
C:Species: Sinapis alba (white mustard)
C:Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jun-2000
C:Accession: S28993
R:Terras, F.R.G.; Torrekens, S.; van Leuven, F.; Osborn, R.W.; Vanderleyden, J.; Cammue, B.A.
FEBS Lett. 316, 233-240, 1993
A:Title: A new family of basic cysteine-rich plant antifungal proteins from Brassicaceae
A:Reference number: S28989; MUID:93138130; PMID:8422949
A:Accession: S28993
A:Molecule type: protein
A:Residues: 1-25 <TER>
C:Superfamily: gamma-thionin

Alignment Scores:

Pred. No.: 6.39e-08 Length: 25
Score: 151.00 Matches: 25
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.08% Indels: 0
DB: 2 Gaps: 0

US-10-006-252A-19 (1-414) x S28993 (1-25)

Qy 103 CAGAACTTGTGGAAAGCCCAAGTGGACATGGTCAGAGTCTGTGGAAACAATAACGCA 162
Db 1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnSerAsnAla 20
Qy 163 TGCAGAAATCAGTGC 177
Db 21 CysLysAsnGlnCys 25

Search completed: May 11, 2004, 17:05:18
Job time : 19.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 11, 2004, 16:57:50 ; Search time 14 Seconds
(without alignments)
3079.578 Million cell updates/sec

Title: US-10-006-252A-19
Perfect score: 752
Sequence: 1 gtttattagtcattgc.....caaaaaaa414

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ n2p model -DEV=xlp
-Q/cn2_1/USPTO_spool_p/US10006252/runat_11052004_141657_22786/app_query.fasta_1.583
-DB=SwissProt_42 -QFMT=fastan -SUFFIX=rs -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START1 -END=1 -MATRIX=Blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=500 -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-CUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10006252 @CN 1 1 16 @runat_11052004_141657_22786 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	442	58.8	80	1 APP1_BRANA	P30225 brassica na
2	417	55.5	80	1 APP2_BRANA	P30230 raphanus sa
3	405	53.9	80	1 APP4_RAPSA	O24331 raphanus sa
4	403	53.6	80	1 APP4_ARATH	Q9f123 arabidopsis
5	400	53.2	80	1 APP3_ARATH	O80994 arabidopsis
6	399	53.1	80	1 APP2_ARATH	O80995 arabidopsis
7	397	52.8	80	1 APP1_ARATH	P30224 arabidopsis
8	394.5	52.5	79	1 APP3_BRANA	Q39313 brassica na
9	393.5	52.3	79	1 APP3_RAPSA	O24332 raphanus sa
10	309	44.1	51	1 APP1_SINAL	P30231 sinapis alb
11	303	40.3	51	1 APP2_SINAL	P30232 sinapis alb
12	233.5	31.1	52	1 APP2_SINAL	Q10989 sinapis alb
13	161	21.4	27	1 APP1_BRANA	P30227 brassica ra
14	149	19.8	161	1 ASF1_HELAN	P22357 helianthus
15	142	18.9	27	1 APP2_BRANA	P30228 brassica ra
16	137	18.2	23	1 APP2_BRANA	P30226 brassica na
17	131.5	17.5	106	1 THG1_NICPA	O24115 nicotiana p
18	114	15.2	105	1 THGF_TOBAC	P30226 nicotiana t

19	109	14.5	75	1 DEF1_CAPAN	Q43413 capsicum an
20	99	13.2	73	1 THG4_ARATH	Q9zu18 arabidopsis
21	95	12.6	75	1 10KD_VIGUN	P18646 vigna ungui
22	93.5	12.4	74	1 DR39_PEA	Q01784 pisum sativ
23	87.5	11.6	72	1 D230_PEA	Q01793 pisum sativ
24	87.5	11.6	735	1 AD02_MOUSE	Q8C718 mus musculu
25	83	11.0	77	1 THG3_ARATH	Q9zu17 arabidopsis
26	82	10.9	77	1 THG1_ARATH	Q39182 arabidopsis
27	81	10.8	74	1 DEF2_CAPAN	O65740 capsicum an
28	80	10.6	46	1 AX2_BETU	P82010 beta vulgar
29	80	10.6	46	1 PSD1_PEA	P81929 pisum sativ
30	80	10.6	77	1 THG2_ARATH	Q19144 arabidopsis
31	80	10.6	833	1 DL_DROME	P10041 drosophila
32	79	10.5	768	1 LEM3_RAT	P98106 rattus norv
33	78.5	10.4	52	1 DEF2_SPIOL	P81571 spinacia ol
34	78	10.4	78	1 THGF_HELAN	P82659 helianthus
35	77	10.2	121	1 ASP2_HELAN	P22184 helianthus
36	77	10.2	2531	1 NTC1_RAT	Q07008 rattus norv
37	76.5	10.2	47	1 PSD2_PEA	P81930 pisum sativ
38	75.5	10.0	1389	1 LTB3_MOUSE	Q8C918 mus musculu
39	75.5	10.0	1713	1 LTBL_MOUSE	Q8C919 mus musculu
40	75	10.0	74	1 P322_SOLTU	P20346 solanum tub
41	74.5	9.9	1429	1 L112_CABEL	P14585 caenorhabdi
42	74.5	9.9	2911	1 FBN2_HUMAN	P35556 homo sapien
43	74	9.8	1408	1 SEER_DROME	P18168 drosophila
44	73.5	9.8	313	1 COXT_KLULA	P78990 kluyveromyc
45	73.5	9.8	1213	1 JAG3_BRARE	Q90y54 brachydanio

ALIGNMENTS

RESULT 1

ID APP1_BRANA STANDARD; PRT; 80 AA.
AC P30225; Q41163;
DT 01-APR-1993 (Rel. 25, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DB Cysteine-rich antifungal protein 1 precursor (APPL).
GN APPL.
OS Brassica napus (Rape), and
OS Raphanus sativus (Radish).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708, 3726;
[1]
RN SV
PP SEQUENCE FROM N.A.
RC SPECIES=Brassica; STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
RX MEDLINE=9529350; PubMed=7780308;
RA Terras F.R.G., Eggermont K., Kovaleva V., Raikhel N.V., Osborn R.W.,
RA Kester A., Rees S.B., Torrekens S., Van Leuven F., Vanderleyden J.,
RA Cammue B.P.A., Broekaert W.F.;
RA "Small cysteine-rich antifungal proteins from radish: their role in
RT host defense."
RT Plant Cell 7:568-573 (1995).
[2]
RN SV
PP SEQUENCE OF 30-73.
RC SPECIES=Brassica; TISSUE=Seed;
RX MEDLINE=93138130; PubMed=8422949;
RA Terras F.R.G., Torrekens S., Van Leuven F., Osborn R.W.,
RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
RA "A new family of basic cysteine-rich plant antifungal proteins from
RT Brassicaceae species."
RT FEBS Lett. 316:233-240 (1993).
[3]
RN SV
PP SEQUENCE OF 30-73.
RC SPECIES=R. sativus; TISSUE=Seed;
RX MEDLINE=92348373; PubMed=1639777;
RA Terras F.R.G., Schoofs H.M.E., de Bolle M.F.C., van Leuven F.,
RA Rees S.B., Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
RA "Analysis of two novel classes of plant antifungal proteins from
RT radish (Raphanus sativus L.) seeds.";

```

RL J. Biol. Chem. 267:15301-15309(1992).
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations.
CC -!- SUBUNIT: Forms oligomers in its native state.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the plant defensin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U18557; AAA69541.1; -
DR PIR; T10176; T10176.
DR HSSP; P30231; LAYJ.
DR InterPro; IPR008176; Gamma-thionin.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.
DR SMART; SM00505; Knot1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
KW Plant defense; Fungicide; Signal; Multigene family;
KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 29
FT CHAIN 30 80 CYSTEINE-RICH ANTIFUNGAL PROTEIN 1.
FT MOD RES 30 30 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 33 80 BY SIMILARITY.
FT DISULFID 44 65 BY SIMILARITY.
FT DISULFID 50 74 BY SIMILARITY.
FT DISULFID 54 76 BY SIMILARITY.
SQ SEQUENCE 80 AA; 8734 MW; 05B90FAAC8DA6C2B CRC64;

Alignment Scores:
Pred. No.: 7,46e-41 Length: 80
Score: 442.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 58.78% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-19 (1-414) x AFPI1_BRANA (1-80)

QY 16 ATGGCTAAGTTTGGCTCCATCGCACTTTCTTCTGCTCTTCTTTCTTTCTGCTCT 75
Db 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaValLeuPheAlaAla 20

QY 76 TTCGAAGCACCACAAATGGTGAAGCAGACAGAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgProSerGlyThrTrp 40

QY 136 TCAGGAGTCTGTGGAACAATAACGATCGAAGATCAGTGCATTAACTTGAGAAGCA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGlnLysAla 60

QY 196 CGACATGATCTTGAACATATGTTCTTCCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
Db 61 ArgHisGlySerCysAsnTy-ValPheProAlaHisLysCysIleCysTyArgPheProCys 80

RESULT 2
APP2_RAPSA STANDARD; PRT; 80 AA.
ID APP2_RAPSA
AC P30230;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 2 precursor (APP2).
GN APP2.
OS Raphanus sativus (Radish).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

```

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OC eurosids II; Brassicales; Brassicaceae; Raphanus.
OX NCBI_TaxID=3726;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
RX MEDLINE=9599350; PubMed=7780308;
RA Terras F.R.G., Eggermont K., Kovaleva V., Raikhel N.V., Osborn R.W.,
RA Kester A., Rees S.B., Torrekens S., van Leuven F., Vanderleyden J.,
RA Cammue B.P.A., Broekaert W.F.;
RT "Small cysteine-rich antifungal proteins from radish: their role in
RT host defense.";
RL Plant Cell 7:573-588(1995).
RN [2]
RP SEQUENCE OF 30-65.
RC TISSUE=Seed;
RX MEDLINE=9234873; PubMed=1639777;
RA Terras F.R.G., Schoofs H.M.E., de Bolle M.P.C., van Leuven F.,
RA Rees S.B., Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
RT "Analysis of two novel classes of plant antifungal proteins from
RT radish (Raphanus sativus L.) seeds.";
RL J. Biol. Chem. 267:15301-15309(1992).
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the plant defensin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U18556; AAA69540.1; -
DR PIR; T10823; T10823.
DR HSSP; P30231; LAYJ.
DR InterPro; IPR008176; Gamma-thionin.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G_Purothionin; 1.
DR SMART; SM00505; Knot1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
KW Plant defense; Fungicide; Signal; Multigene family;
KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 29
FT CHAIN 30 80 CYSTEINE-RICH ANTIFUNGAL PROTEIN 2.
FT MOD RES 30 30 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 33 80 BY SIMILARITY.
FT DISULFID 44 65 BY SIMILARITY.
FT DISULFID 50 74 BY SIMILARITY.
FT DISULFID 54 76 BY SIMILARITY.
SQ SEQUENCE 80 AA; 8875 MW; 746110D9A8CE6370 CRC64;

Alignment Scores:
Pred. No.: 4,36e-38 Length: 80
Score: 417.00 Matches: 74
Percent Similarity: 95.00% Conservative: 2
Best Local Similarity: 92.50% Mismatches: 4
Query Match: 55.45% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-19 (1-414) x APP2_RAPSA (1-80)

QY 16 ATGGCTAAGTTTGGCTCCATCGCACTTTCTTCTGCTCTTCTTTCTTTCTGCTCT 75
Db 1 MetAlaLysPheAlaSerIleAlaLeuPheAlaValLeuPheAlaAla 20

QY 76 TTCGAAGCACCACAAATGGTGAAGCAGACAGAGTTGTGCGAAAGGCCAAGTGGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGlnArgProSerGlyThrTrp 40

QY 136 TCAGGAGTCTGTGGAACAATAACGATCGAAGATCAGTGCATTAACTTGAGAAGCA 195

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Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluLysAla 60
QY 196 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255
Db 61 ArgHisGlySerCysAsnTyrrValPheProAlaHisLysCysIleCysTyrPheProCys 80

RESULT 3
APP4_RAPSA
ID APP4_RAPSA STANDARD; PRT; 80 AA.
AC Q2431;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteine-rich antifungal protein 4 precursor (APP4).
GN APP4.
OS Raphanus sativus (Radish).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Raphanus.
OX NCBI_TaxID=3726;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Ronde Rode Kleine Witpunt; TISSUE=Seed;
RA Terras F.R.G., Goderis I.J., Penninckx I.J., Osborn R.W.,
RA Broekaert W.F.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the plant defensin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X97318; CAA65983.1; -.
CC FR; T10183; T10183.
CC HSP; P30231; IAYU.
CC InterPro: IPR008176; Gamma-thionin.
CC Pfam; PF003614; Knot1.
CC ProDom; PD002594; G_Purothionin; 1.
CC SMART; SM00505; Knot1; 1.
CC PROSITE; PS00940; GAMMA_THIONIN; 1.
CC Plant defense; Fungicide; Signal; Multigene family;
CC Pyrrolidone carboxylic acid.
CC SIGNAL 1 29 POTENTIAL.
CC CHAIN 30 80 CYSTEINE-RICH ANTIFUNGAL PROTEIN 4.
CC MOD_RES 30 30 PYRROLIDONE CARBOXYLIC ACID (BY
CC SIMILARITY).
CC FT DISULFID 33 80 BY SIMILARITY.
CC FT DISULFID 44 65 BY SIMILARITY.
CC FT DISULFID 54 76 BY SIMILARITY.
CC FT DISULFID 54 76 BY SIMILARITY.
CC SQ SEQUENCE 80 AA; 8873 MW; B5F667B6441818C9 CRC64;

Alignment Scores:
Pred. No.: 9,26e-37 Length: 80
Score: 405.00 Matches: 72
Percent Similarity: 92.50% Conservative: 2
Best Local Similarity: 90.00% Mismatches: 6
Query Match: 53.86% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-19 (1-414) x APP4_RAPSA (1-80)

QY 16 ATGGCTAAGTTGCGTCCATCGACATCTTTTGGCTGCTGCTTTGCTGCTGCT 75

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Db 1 MetAlaLysPheValSerIleIleThrLeuLeuPheValAlaLeuValLeuPheAlaLa 20
QY 76 TTCGAAGCCCAACAATGTTGGAAGCACAGAAAGTTGTGCGAAAGCCCAAGTGGACATGG 135
Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluArgSerSerGlyThrTrp 40
QY 136 TCAGGAGTCTGTCGAAACAATAACGATGCAAGATCAAGTCAGTCATTAACTTCAGAAACA 195
Db 41 SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
QY 196 CGACATGGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTGT 255
Db 61 ArgHisGlySerCysAsnTyrrIlePheProTyrHisArgCysIleCysTyrPheProCys 80

RESULT 4
APP4_ARATH
ID APP4_ARATH STANDARD; PRT; 80 AA.
AC Q9F123; P82786;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable cysteine-rich antifungal protein LCR77 precursor (APP).
GN LCR77 OR AT5G44420 OR MFC16.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RC MEDLINE=99397451; PubMed=10470850;
RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.
RT Sequence features of the regions of 1,011,550 bp covered by seventeen
RT P1 and TAC clones."
RL DNA Res. 6:183-195(1999).
RN [2]
RP IDENTIFICATION.
RA Vancosthuyse V., Mieg C., Dumas C., Cock J.M.;
RL Submitted (JUN-2000) to Swiss-Prot.
CC -1- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the plant defensin family.
CC
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CC
CC EMBL; AB017065; BAB09149.1; -.
CC HSP; P30231; IAYU.
CC InterPro: IPR008176; Gamma-thionin.
CC InterPro: IPR003614; Knot1.
CC Pfam; PF00304; Gamma-thionin; 1.
CC ProDom; PD002594; G_Purothionin; 1.
CC SMART; SM00505; Knot1; 1.
CC PROSITE; PS00940; GAMMA_THIONIN; 1.
CC Plant defense; Fungicide; Signal; Multigene family;
CC Pyrrolidone carboxylic acid.
CC SIGNAL 1 29 POTENTIAL.
CC CHAIN 30 80 PROBABLE CYSTEINE-RICH ANTIFUNGAL PROTEIN
CC LCR77.
CC MOD_RES 30 30 PYRROLIDONE CARBOXYLIC ACID (BY
CC SIMILARITY).
CC FT DISULFID 33 80 BY SIMILARITY.
CC FT DISULFID 44 65 BY SIMILARITY.
CC FT DISULFID 50 74 BY SIMILARITY.

```

FT DISULFID 54 76 BY SIMILARITY.
SQ SEQUENCE 80 AA; 8518 MW; 2D0DAFB38E9B6321 CRC64;
Alignment Scores:
Pred. No.: 1 54e-36 Length: 80
Score: 403.00 Matches: 71
Percent Similarity: 95.00% Conservative: 5
Best Local Similarity: 88.75% Mismatches: 4
Query Match: 53.59% Indels: 0
DB: 1 Gaps: 0
US-10-006-252A-19 (1-414) x APP4_ARATH (1-80)
QY 16 ATGGCTAAGTTTCGTCATCGCACTTCTTTTGTGCTGCTCTTTTGTGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleThrLeuIlePheAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAAGCACCACAAATGCTGGAAGCACAGAAAGTTGTGCGAAAGCCCAAGTGGACATGG 135
Db 21 PheAspAlaProAlaMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTIP 40
QY 136 TCAGGAGTCTGTGGAACAAATACGATCGCAGATCATGTCATTAACCTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
QY 196 CGACATGGATCTTGCACATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80
RESULT 5
APP3_ARATH STANDARD; PRT; 80 AA.
ID APP3_ARATH
AC O80994;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable cysteine-rich antifungal protein At2g26020 precursor (AFP).
GN AT2g26020 OR T19L18.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsi.
ON NCBI_TaxID=3702;
RX STRAIN=cv. Columbia;
RC MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT thaliana.";
RL Nature 402:761-768(1999).
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the plant defensin family.
CC
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CC
CC EMBL: AC004747; AAC31244.1; -.
DR PIR: T02621; T02621.

HSP: P30231; IAYJ.
DR InterPro; IPR008176; Gamma-thionin.
DR InterPro; IPR003614; Knot1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G-Purothionin; 1.
DR SMART; SM00505; Knot1; 1.
DR PROSITE; PS00940; GAMMA THIONIN; 1.
KW Plant defense; Fungicide; Signal; Multigene family;
KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 80 PROBABLE CYSTEINE-RICH ANTIFUNGAL PROTEIN
FT MOD_RES 30 30 AT2G26020.
FT PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT DISULFID 33 80 BY SIMILARITY.
FT DISULFID 44 65 BY SIMILARITY.
FT DISULFID 50 74 BY SIMILARITY.
FT DISULFID 54 76 BY SIMILARITY.
SQ SEQUENCE 80 AA; 8640 MW; 81B106058BAFFC7 CRC64;
Alignment Scores:
Pred. No.: 3 31e-36 Length: 80
Score: 400.00 Matches: 70
Percent Similarity: 93.75% Conservative: 5
Best Local Similarity: 87.50% Mismatches: 5
Query Match: 53.19% Indels: 0
DB: 1 Gaps: 0
US-10-006-252A-19 (1-414) x APP3_ARATH (1-80)
QY 16 ATGGCTAAGTTTCGTCATCGCACTTCTTTTGTGCTGCTCTTTTGTGCTGCT 75
Db 1 MetAlaLysPheAlaSerIleThrLeuIlePheAlaLeuValLeuPheAlaAla 20
QY 76 TTCGAAGCACCACAAATGCTGGAAGCACAGAAAGTTGTGCGAAAGCCCAAGTGGACATGG 135
Db 21 PheGluValProThrMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTIP 40
QY 136 TCAGGAGTCTGTGGAACAAATACGATCGCAGATCATGTCATTAACCTTGAGAAAGCA 195
Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
QY 196 CGACATGGATCTTGCACATGCTTCCAGCTCACAAGTGTATCTGCTACTTCTTGT 255
Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80
RESULT 6
APP2_ARATH STANDARD; PRT; 80 AA.
ID APP2_ARATH
AC O80955;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable cysteine-rich antifungal protein At2g26010 precursor (AFP).
GN AT2G26010 OR T19L18.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsi.
ON NCBI_TaxID=3702;
RX STRAIN=cv. Columbia;
RC MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT thaliana.";
RL Nature 402:761-768(1999).
CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
CC cations (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the plant defensin family.
CC
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CC
CC EMBL: AC004747; AAC31244.1; -.
DR PIR: T02621; T02621.

RT thaliana.";
 RL Nature 402:761-768(1999).
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 CC
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 CC
 CC EMBL; AC004747; AAC31234.1; -
 DR PIR; T02622; T02622.
 DR HSP; P30231; 1AVT.
 DR InterPro; IPR008176; Gamma-thionin.
 DR InterPro; IPR003614; Knott.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G.Purethionin; 1.
 DR SMART; SM00505; Knott1; 1.
 DR PROSITE; PS00940; GAMMA THIONIN; 1.
 KW Plant defense; Fungicide; Signal; Multigene family;
 KW Pyrrolidone carboxylic acid.
 FT SIGNAL 1 29
 FT CHAIN 30 80
 FT
 FT MOD_RES 30 30
 FT
 FT DISULFID 33 80
 FT DISULFID 44 65
 FT DISULFID 50 74
 FT DISULFID 54 76
 FT
 FT SQ SEQUENCE 80 AA; 8580 MW; 99E1E0D4443AD67B CRC64;
 Alignment Scores:
 Pred. No.: 4.27e-36 Length: 80
 Score: 399.00 Matches: 71
 Percent Similarity: 93.75% Conservative: 4
 Best Local Similarity: 88.75% Mismatches: 5
 Query Match: 53.06% Indels: 0
 DB: 1 Gaps: 0
 US-10-006-252a-19 (1-414) x APP2_ARATH (1-80)
 Qy 16 ATGGCTAAGTTGGTCCATCATCGCACATCTTTTGTGCTGCTGCTTTTGTGCTGCT 75
 Db 1 MetAlalysSerAlaIleIleThrPheLeuPheAlaLeuValLeuPheAlaala 20
 Qy 76 TTCGAGCACCAACATGTGTGGAGCACAGAGTGTGCGAAGGCCAAGTGGGACATGG 135
 Db 21 PheGluAlaProIleMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40
 Qy 136 TCAGGAGTGTGGACACATACCGATCAGCATCAGATCAGTGCATTAACTTGAGAAACA 195
 Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
 Qy 196 CGACATGGATTTGCAACTATGTCTTCCAGGTCAACAGTGTATCTGTACTTTCTCTGT 255
 Db 61 LysHisGlySerCysAsnTrpValPheProAlaHisLysCysIleCysTrpPheProCys 80
 RESULT 7
 APP1_ARATH
 ID APP1_ARATH STANDARD; PRT; 80 AA.
 AC P30224; Q42179;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 1 precursor (APP1) (Anther-specific
 DE protein S18 homolog).
 GN APP1 OR PDI1.1 OR AT1G75830 OR T4012.6 OR T4012.7.

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Raynal M., Grellot F., Laudie M., Meyer Y., Cooke R., Delseny M.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=Seed;
 RA Raynal M.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99178804; PubMed=10080719;
 RA Williams R.W., Clark S.E., Meyerowitz E.M.;
 RT "Genetic and physical characterization of a region of Arabidopsis
 RL chromosome 1 containing the CLAVATA1 gene.";
 RN Plant Mol. Biol. 39:171-176(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buchler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Dunn P., Etny P., Feldblyum T.V., Feng J.-D., Pong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koc H.S., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marzilli A.,
 RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tamunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RL thaliana.";
 RN Nature 408:816-820(2000).
 RN [5]
 RP SEQUENCE OF 30-56.
 RC TISSUE=Seed;
 RX MEDLINE=93138130; PubMed=8422949;
 RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.P.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RL Brassicaceae species.";
 CC FEBS Lett. 316:233-240(1993).
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -!- SUBUNIT: Forms oligomers in its native state.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 CC
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 CC
 CC EMBL; Z27258; CAA81770.1; -
 DR EMBL; Z29957; CAA82845.1; -
 DR EMBL; X91916; CAA63009.1; -
 DR EMBL; AF049870; AAD02502.1; -
 DR EMBL; AC007396; AAF26754.1; -

[illegible]

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EMBL; X97319;	CXA65984.1;	-
PIR; T10243;	T10243.	
HSSP; F30231;	1AYJ.	
InterPro; IPR008176;	Gamma-thionin.	
InterPro; IPR003614;	Knot1.	
Pfam; PF003104;	Gamma-thionin; 1.	
ProDom; PD002594;	G_Purothionin; 1.	
SMART; SMC0505;	Knot1; 1.	
PROSITE; PS00940;	GAMMA-THIONIN; 1.	
Plant defense; Fungicide; Signal;	Multigene family.	
SIGNAL	1	29 POTENTIAL.
CHAIN	30	79 CYS(TEINE)-RICH ANTIFUNGAL PROTEIN 3.
DISULFID	32	79 BY SIMILARITY.
DISULFID	43	64 BY SIMILARITY.
DISULFID	49	73 BY SIMILARITY.
DISULFID	53	75 BY SIMILARITY.
SEQUENCE	79 AA;	8479 MW; BAF80465DBD48548 CRC64;
SQ		

Alignment Scores:	
Pred. No.:	1.72e-35
Score:	393.50
Percent Similarity:	95.00%
Best Local Similarity:	90.00%
Query Match:	52.33%
DB:	1
Length:	79
Matches:	72
Conservative:	4
Mismatches:	3
Indels:	1
Gaps:	1

US-10-006-252A-19 (1-414) x AFP3 RAPSA (1-79)

16	ATGGCTAAGTTTGGTCATCATCGCACTCTCTTTTGTCTGCTCTCTTTTGTCTGCT	75
	:::::	
1	MetAlaLysPheAlaSerIleValAlaLeuLeuPheAlaAlaLeuValValPheAlaAla	20
	:::::	
76	TTCGAAGCACCAACAATTGGTGGAAGCACAGAAGTTGTGCAAAGGCCAAGTGGGACATGG	135
	:::::	
21	PheGluAlaProThrValValGluAla---LysLeuCysGluArgSerGlyThrTrp	39
	:::::	
136	TCAGAGTCTCTGGAAACAATAAGCATGCAAGAATCAGTGCATTAACTTGAGAAAGCA	195
	:::::	
40	SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleArgLeuGluGlyAla	59
	:::::	
196	CGCATGGATCTTCGAACATATGTCTCCAGCTCACAAGTGTATCTGCTACTTTCTCTGT	255
	:::::	
60	GlnHisGlySerCysAsnTyrlValPheProAlaHisLysCysIleCyslvsrVsrPheProCys	79
	:::::	

RESULT 10	APFPI_SINAL	APFPI_SINAL	STANDARD;	PRT;	51 AA.
ID	AC	P30231;			
DT	01-APR-1993	(Rel. 25, Created)			
DT	01-OCT-1996	(Rel. 34, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DE	Cysteine-rich antifungal protein 1 (APF1) (M1).				
OS	Sinapis alba (white mustard) (Brassicaceae).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;				
OC	eucrotsids II; Brassicales; Brassicaceae; Sinapis.				
OX	NCBI TaxID=3728;				

(iii)
SEQUENCE.
TISUP=Seed;
MEDLINE=95433791; PubMed=8836771;
Neumann G.M., Condron R., Polya G.M.;
"Purification and mass spectrometry-based sequencing of yellow
mustard (Sinapis alba L.) 6 kDa proteins. Identification as

```

RT  antifungal proteins." ;
Int. J. Pept. Protein Res. 47:437-446(1996).
RN  [2]
RC  SEQUENCE OF 1-25.
RX  TISSUE=Seed;
RA  MEDLINE=93138130; PubMed=8422949;
RA  Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
RA  Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
RT  "A new family of basic cysteine-rich plant antifungal proteins from
RT  Brassicaceae species.";
RL  FEBS Lett. 316:233-240(1993).
RN  [3]
RX  STRUCTURE BY NMR.
RP  MEDLINE=98300344; PubMed=9636715;
RA  Fant F., Franken W.F., Broekaert W.F., Borremans F.A.M.;
RT  "Determination of the three-dimensional solution structure of Raphanus
RT  sativus antifungal protein 1 by 1H NMR.";
RL  J. Mol. Biol. 279:257-270(1998).
CC  - FUNCTION: Possesses antifungal activity sensitive to inorganic
CC  cations.
CC  - SUBUNIT: Forms oligomers in its native state.
CC  - MASS SPECTROMETRY: MW=5677; MW_ERR=1.0; METHOD=Electrospray.
CC  - SIMILARITY: Belongs to the plant defensin family.
CC  PDB; 1AYJ; 28-JAN-98.
DR  InterPro; IPR008176; Gamma-thionin.
DR  InterPro; IPR003614; Knott1.
DR  Pfam; PF00304; Gamma-thionin; 1.
DR  ProDom; PD002594; G_Purothionin; 1.
DR  SMART; SM00505; Knott1; 1.
DR  PROSITE; PS00940; GAMMA_THIONIN; 1.
KW  Plant defense; Fungicide; 3D-structure; Pyrrolidone carboxylic acid.
DR  MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT  DISULFID 4 51
FT  DISULFID 15 36
FT  DISULFID 21 45
FT  DISULFID 25 47
FT  STRAND 4 7
FT  HELIX 18 28
FT  STRAND 34 37
FT  STRAND 44 49
SQ  SEQUENCE 51 AA; 5695 MW; 770990E72DD1C469 CRC64;

Alignment Scores:
Pred. No.: 3,75e-26 Length: 51
Score: 309.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.09% Indels: 0
DB: 1 Gaps: 0

US-10-006-252A-19 (1-414) x AFP1_SINAL (1-51)
QY 103 CAGAAGTGTGCGAAGCGGCAAGTCAGGAGCATGTCAGGAGTCTGTGGAAACAATAACGCA 162
Ddb 1 GlnlyLeuCySGluArgProSerGlyThrTpSerGlyValCysGlyAsnAsnAla 20

163 TCGAAGAATCAGTGCATTAACCTTGAGAAGCACACACATGGATCTTGGCAACTATGCTCTTC 222
Ddb 21 CyslysaSngLnCyslleaSenLeuGluLyAlaAaGHisGlySerCysasnIyrValPhe 40

223 CCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 255
Ddb 41 ProAlaHisLysCysileCystyrPheProCys 51

RESULT 11
AF2A_SINAL
UID AF2A_SINAL STANDARD; PRT; 51 AA.
AC P0232;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
OS Cysteine-rich antifungal protein 2A (AFP2A) (M2A).
OS Sinapis alba (white mustard) (Brassica hirta)

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids II; Brassicales; Brassicaceae; Sinapis.
 OX NCBI_TaxID=3728;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=96433791; PubMed=8836771;
 RA Neumann G.M., Condron R., Polya G.M.;
 RT "Purification and mass spectrometry-based sequencing of yellow
 RT mustard (Sinapis alba L.) 6 kDa proteins. Identification as
 RT antifungal proteins.";
 RL Int. J. Pept. Protein Res. 47:437-446(1996).
 RN [2]
 RP SEQUENCE OF 1-26.
 RC TISSUE=Seed;
 RX MEDLINE=93138130; PubMed=8422949;
 RA Terras F.R.G., Torrekens S., van Leeuwen F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.;
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RT Brassicaceae species.";
 RL FEBS Lett. 316:233-240(1993).
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -!- SUBUNIT: Forms oligomers in its native state.
 CC -!- MASS SPECTROMETRY: MW=5705; MW.PRR=0.8; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 DR HSP: P30231; 1AUV.
 DR InterPro: IPR008176; Gamma-thionin.
 DR InterPro: IPR003614; Krot1.
 DR Pfam: PF00304; Gamma-thionin; 1.
 DR ProDom: PD002594; G_Purothionin; 1.
 DR SMART: SM00505; Krot1; 1.
 DR PROSITE: PS00940; GAMMA THIONIN; 1.
 DR Fungicide; Phosphorylation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 4 51 BY SIMILARITY.
 FT DISULFID 15 36 BY SIMILARITY.
 FT DISULFID 21 45 BY SIMILARITY.
 FT DISULFID 25 47 BY SIMILARITY.
 SQ SEQUENCE 51 AA; 5722 MW; 1C7F50E72DC945B1 CRC64;

Alignment Scores:

Pred. No.: 1.73e-25 Length: 51
 Score: 303.00 Matches: 49
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 96.08% Mismatches: 0
 Query Match: 40.29% Indels: 0
 DB: 1 Gaps: 0

US-10-006-252a-19 (1-414) x AF2A_SINAL (1-51)

QY 103 CAGAGTTGTCGAAAGCCAGTGGACATGTCAGGAGTGTGGAAACAAATACCA 162
 Db 1 GlnLysLeuCysGlnArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
 QY 163 TGCAGATCATGTCATTAACTTGCAGACGACGATGCTTGCACACTATGCTTC 222
 Db 21 CysArgAsnGlnCysIleAsnLeuGluLeuAlaArgHisGlySerCysAsnTrpValPhe 40
 QY 223 CAGCTCAAGTGTATCTGCTACTTTCCTTGT 255
 Db 41 ProAlaHisLysCysIleCysTyrPheProCys 51

RESULT 12

AF2B_SINAL
 ID AF2B_SINAL STANDARD; PRT; 52 AA.
 AC Q10989;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 2B (APP2B) (M2B).

OS Sinapis alba (White mustard) (Brassica hirta).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids II; Brassicales; Brassicaceae; Sinapis.
 OX NCBI_TaxID=3728;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=96433791; PubMed=8836771;
 RA Neumann G.M., Condron R., Polya G.M.;
 RT "Purification and mass spectrometry-based sequencing of yellow
 RT mustard (Sinapis alba L.) 6 kDa proteins. Identification as
 RT antifungal proteins.";
 RL Int. J. Pept. Protein Res. 47:437-446(1996).
 RN [2]
 RP SEQUENCE OF 1-26.
 CC -!- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -!- SUBUNIT: Forms oligomers in its native state.
 CC -!- MASS SPECTROMETRY: MW=5840; MW.PRR=1.2; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the plant defensin family.
 DR HSP: P30231; 1AUV.
 DR InterPro: IPR008176; Gamma-thionin.
 DR InterPro: IPR003614; Krot1.
 DR Pfam: PF00304; Gamma-thionin; 1.
 DR ProDom: PD002594; G_Purothionin; 1.
 DR SMART: SM00505; Krot1; 1.
 DR PROSITE: PS00940; GAMMA THIONIN; FALSE NEG.
 KW Fungicide; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
 FT DISULFID 4 52 BY SIMILARITY.
 FT DISULFID 16 37 BY SIMILARITY.
 FT DISULFID 22 46 BY SIMILARITY.
 FT DISULFID 26 48 BY SIMILARITY.
 SQ SEQUENCE 52 AA; 5856 MW; A060FCBC13A8D1FB CRC64;

Alignment Scores:

Pred. No.: 8.48e-18 Length: 52
 Score: 233.50 Matches: 40
 Percent Similarity: 84.62% Conservative: 4
 Best Local Similarity: 76.92% Mismatches: 7
 Query Match: 31.05% Indels: 1
 DB: 1 Gaps: 1

US-10-006-252a-19 (1-414) x AF2B_SINAL (1-52)

QY 103 CAGAGTTGTCGAAAGCCAGTGGACATG---TCAGAGTCTGTGAAACAAATAC 159
 Db 1 GlnLysLeuCysAlaArgProSerGlyThrTrpSerGlyAsnCysArgAsnAsn 20
 QY 160 GCATGCAAGATCATGTCATTAACTTGCAGACGACGATGCTTGCACACTATGTC 219
 Db 21 AlaCysArgAsnPheCysIleLysLeuGluLysSerArgHisGlySerCysAsnIlePro 40
 QY 220 TTCAGCTCAAGTGTATCTGCTACTTTCCTTGT 255
 Db 41 PheProSerAsnLysCysIleCysTyrPheProCys 52

RESULT 13

AFPL_BRARA
 ID AFPL_BRARA STANDARD; PRT; 27 AA.
 AC P30227;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 1 (APPL) (Fragment).
 OS Brassica rapa (Turnip).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids II; Brassicales; Brassicaceae; Brassica.

NCBI_TaxID=51350;

[1]

SEQUENCE.

RC TISSUE=Seed;

RX MEDLINE=93138130; PubMed=8422949;

RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.,
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RT Brassicaceae species.";
 RL FEBS Lett. 316:233-240(1993).
 CC -1- FUNCTION: Possesses antifungal activity sensitive to inorganic
 CC cations.
 CC -1- SUBUNIT: Forms oligomers in its native state.
 CC -1- SIMILARITY: Belongs to the plant defensin family.
 CC PIR; S28989; S28989.
 DR HSP; P30231; IAYJ.
 DR InterPro; IPR008176; Gamma-thionin.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G Purothionin; 1.
 DR PROSITE; PS00940; GAMMA_THIONIN; 1.
 KW Plant defense; Fungicide; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 27 27
 SQ SEQUENCE 27 AA; 2925 MW; 4C85BD9C611D4A9E CRC64;
 Alignment Scores:
 Pred. No.: 8.5e-10 Length: 27
 Score: 161.00 Matches: 27
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 21.41% Indels: 0
 DB: 0 Gaps: 0
 US-10-006-252A-19 (1-414) x APPI_BRARA (1-27)
 QY 103 CAGAGTTGCGAAGCCAGTGGGACATGTCAGAGTCTGTGGAAACAATAACGCA 162
 Db 1 GlnLysLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAla 20
 QY 163 TGCAGAAATCACTGCAATTAAC 183
 Db 21 CysLysAsnGlnCysIleAsn 27
 RESULT 14
 ASFL_HELAN
 ID _ASFL1_HELAN STANDARD; PRT; 161 AA.
 AC P22357;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Anther-specific protein SF18 precursor (Fragment).
 OS Helianthus annuus (Common sunflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC campanulids; Asterales; Asteraceae; Asteroidae; Heliantheae;
 OC Helianthus.
 OC NCBI_TaxID=4232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. HA401B / Cargill; TISSUE=Anther;
 RX MEDLINE=91338702; PubMed=2102380;
 RA Domon C., Evrard J.-L., Herdenberger F., Pillay D.T.N., Steinmetz A.;
 RT "Nucleotide sequence of two anther-specific cDNAs from sunflower
 (Helianthus annuus L.).";
 RL Plant Mol. Biol. 15:643-646(1990).
 CC -1- FUNCTION: Anther-specific cell wall protein which could contribute
 CC to the cell wall architecture of epidermal anther cells via
 CC intermolecular disulfide bridges.
 CC -1- TISSUE SPECIFICITY: Epidermal anther cells.
 CC -1- DEVELOPMENTAL STAGE: Late developmental stages.
 CC -1- SIMILARITY: Belongs to the plant defensin family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC EMBL; X53375; CAA37455.1; -.
 DR PIR; S12246; S12246.
 DR HSP; P30231; IAYJ.
 DR InterPro; IPR008176; Gamma-thionin.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G Purothionin; 1.
 DR SMART; SM00505; Knot1; 1.
 DR PROSITE; PS00940; GAMMA_THIONIN; 1.
 KW Signal; Cell wall.
 FT NON_TER 1 1
 FT SIGNAL <1 8
 FT CHAIN 9 161 ANTER-SPECIFIC PROTEIN SF18.
 FT DOMAIN 9 65 GAMMA-THIONIN LIKE DOMAIN.
 FT DOMAIN 70 161 PROLINE DOMAIN.
 FT DISULFID 18 65 BY SIMILARITY.
 FT DISULFID 29 50 BY SIMILARITY.
 FT DISULFID 35 59 BY SIMILARITY.
 FT DISULFID 39 61 BY SIMILARITY.
 SQ SEQUENCE 161 AA; 15363 MW; 27A9CF4633ADA02B CRC64;
 Alignment Scores:
 Pred. No.: 2.06e-08 Length: 161
 Score: 149.00 Matches: 23
 Percent Similarity: 64.00% Conservative: 9
 Best Local Similarity: 46.00% Mismatches: 18
 Query Match: 19.81% Indels: 0
 DB: 1 Gaps: 0
 US-10-006-252A-19 (1-414) x ASFL_HELAN (1-161)
 QY 106 AGCTTGTGCAAGCCAGTGGGACATGTCAGAGTCTGTGGAAACAATAACGCAATGC 165
 Db 16 LysileCysGlnLysProSerLysThrTrpSerGlyValCysGlyAsnAsnAla 20
 QY 166 AAGAATCACTGCAATTAACCTTGGAAAGCAGACATGTCAGAGTCTGTGGAAACAATAACGCAATGC 225
 Db 36 AspLysArgCysIleAsnTrpGluGlyAlaLysHisGlyAlaCysHisGlnArgGluAla 55
 QY 226 GCTCACAGTGTATCTGCTACTTCTCTGT 255
 Db 56 LysHisMetCysPheCysTyrPheAspCys 65
 RESULT 15
 APP2_BRARA
 ID _APP2_BRARA STANDARD; PRT; 27 AA.
 AC P30228;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteine-rich antifungal protein 2 (APP2) (Fragment).
 OS Brassica rapa (Turnip).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids II; Brassicales; Brassicaceae; Brassica.
 OC NCBI_TaxID=51350;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=93138130; PubMed=8422949;
 RA Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
 RA Vanderleyden J., Cammue B.P.A., Broekaert W.F.,
 RT "A new family of basic cysteine-rich plant antifungal proteins from
 RT Brassicaceae species.";
 RL FEBS Lett. 316:233-240(1993).
 CC -1- FUNCTION: Possesses some antifungal activity sensitive to
 CC inorganic cations and antibacterial activity against B.megaterium.
 CC -1- SUBUNIT: Forms oligomers in its native state.
 CC -1- SIMILARITY: Belongs to the plant defensin family.
 DR PIR; S28990; S28990.
 DR HSP; P30231; IAYJ.

DR InterPro: IPR008176; Gamma-thionin.
 DR ProDom: PD002594; G_Parothionin; 1.
 DR ProSITE: PS00940; GAMMA_THIONIN; 1.
 KW Plant defense; Fungicide; Antibiotic; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT UNSURE 27 27
 FT NON TER 27 27
 SQ SEQUENCE 27 AA; 2891 MW; 571E6D9C611D4A9E CRC64;

Alignment Scores:
 Pred. No.: 1,07e-07 Length: 27
 Score: 142.00 Matches: 25
 Percent Similarity: 96.15% Conservative: 0
 Best Local Similarity: 96.15% Mismatches: 1
 Query Match: 18.88% Indels: 0
 DB: 1 Gaps: 0

US-10-006-252A-19 (1-414) X APP2_BRARA (1-27)

Qy 103 CAGAGTTTGTGGAAAGCCAGTCGGACATGTCAGGAGTCTGTGGAACATAACGCA 162
 Db 1 GlnLysLeuCysGluArgProSerGlyThr***SerGlyValCysGlyAsnAsnAla 20
 Qy 163 TGCAGAAATCAGTGCATT 180
 Db 21 CysLysAsnGlnCysIle 26

Search completed: May 11, 2004, 17:03:07
 Job time : 29 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 11, 2004, 16:58:28 ; Search time 41 Seconds

(without alignments)

6371.929 Million cell updates/sec

Title: US-10-006-252A-19

Perfect score: 752

Sequence: 1 gttttattgtatcgtgc.....caaaaaaaaaaaaaaaaaaaaa 414

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DBV=xlp
-Q=/cgn2_1/USPTO.spool_p/US10006252/runat_11052004_141657_22797/app_query.fasta_1.583
-DB=SPREMBL 25 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptio -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10006252.cgn_1_1_86/runat_11052004_141657_22797 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rv:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	421	56.0	80	10	Q94IN7	Q94in7 Brassica o1

2	407	54.1	80	10	Q9FS38	Q9fs38 eutrema was
3	402	53.5	80	10	Q8H6K0	Q8h6k0 brassica ra
4	398	52.9	80	10	Q9FI22	Q9fi22 arabidopsis
5	207	27.5	80	10	Q9FZ31	Q9fz31 arabidopsis
6	181	24.1	78	10	Q8VZQ7	Q8vzq7 arabidopsis
7	164	21.8	56	10	Q9FWR6	Q9fwr6 arabidopsis
8	153.5	20.4	108	10	Q8LSM8	Q8lsm8 helianthus
9	141.5	18.8	105	10	Q40128	Q40128 lycopersico
10	139.5	18.6	132	10	Q842X5	Q842x5 artenisia v
11	118	15.7	83	10	Q8GTL2	Q8gtl2 picea abies
12	116	15.4	105	10	Q8GTM0	Q8gtm0 nicotiana a
13	115	15.3	83	10	Q40779	Q40779 picea abies
14	114	15.2	105	10	Q24105	Q24105 nicotiana e
15	112	14.9	75	10	Q8W434	Q8w434 vigna radia
16	110.5	14.7	83	10	Q40539	Q40539 nicotiana t
17	109	14.5	101	10	Q8H600	Q8h600 petunia hyb
18	108	14.4	77	10	Q82788	Q82788 arabidopsis
19	107.5	14.3	87	10	Q948T3	Q948t3 pyrus pyrif
20	103.5	13.8	81	10	Q948T2	Q948t2 pyrus pyrif
21	100	13.3	103	10	Q8H6Q1	Q8h6q1 petunia hyb
22	95.5	12.7	87	10	Q948T4	Q948t4 pyrus pyrif
23	94.5	12.6	107	10	Q9XHE3	Q9xhe3 capsicum ch
24	93.5	12.4	76	10	Q8LEG6	Q8leg6 arabidopsis
25	92	12.2	108	10	Q82789	Q82789 arabidopsis
26	91.5	12.2	81	10	Q422Z5	Q422z5 cryza sativ
27	90.5	12.1	380	10	Q49590	Q49590 arabidopsis
28	86.5	11.5	72	10	Q9FR81	Q9fr81 pisum sativ
29	86.5	11.5	78	10	Q8W4V6	Q8w4v6 capsicum an
30	85.5	11.4	81	10	Q82756	Q82756 arabidopsis
31	85	11.3	79	10	Q24104	Q24104 nicotiana e
32	85	11.3	217	13	P70016	P70016 xenopus lae
33	82.5	11.0	76	10	Q82732	Q82732 arabidopsis
34	82.5	11.1	221	5	Q20860	Q20860 caenorhabdi
35	81.5	10.8	79	10	Q99807	Q99807 glycine max
36	81	10.8	78	10	Q9MB66	Q9mb66 nicotiana t
37	81	10.8	82	10	Q8L698	Q8l698 triticum ae
38	80.5	10.7	84	10	Q9SEMA	Q9sem4 capsicum an
39	79	10.5	60	10	Q8H6L2	Q8h6l2 pisum sativ
40	79	10.5	77	10	Q39403	Q39403 brassica ca
41	79	10.5	77	10	Q24094	Q24094 medicago tr
42	79	10.5	794	5	Q8T4P0	Q8t4p0 lytechinus
43	79	10.5	1065	11	Q810H2	Q810h2 mus musculu
44	78.5	10.5	715	5	Q9NAP6	Q9nap6 caenorhabdi
45	78	10.4	88	10	Q94A28	Q94a28 arabidopsis

ALIGNMENTS

RESULT 1					
Q94IN7	Q94IN7	PRELIMINARY;	PRT;	80 AA.	
AC	Q94IN7;				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DE	Defensin precursor.				
GN	DEF.				
OS	Brassica oleracea (Cauliflower).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;				
OC	eurosid II; Brassicales; Brassicaceae; Brassica.				
OX	NCBI_TaxID=3712;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Esnault R.;				
RT	"Brassica oleracea def gene for defensin.";				
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AJ311046; CAC37558.1;				
DR	GO; GO:0003793; F:defense/immunity protein activity; IEA.				
DR	InterPro; IPR008176; Gamma-thionin.				
DR	InterPro; IPR003614; Knott1.				
DR	Pfam; PF00304; Gamma-thionin; 1.				
DR	ProDom; PD002594; G_Purothionin; 1.				

Alignment Scores:		
Pred. No.:	2.57e-39	Length: 80
Score:	407.00	Matches: 72
Percent Similarity:	96.25%	Conservative: 5
Best Local Similarity:	90.00%	Mismatches: 3
Query Match:	94.12%	Indels: 0

US-10-006-252A-19 (1-414) x Q8H6K0 (1-80)

Qy	16	ATCGCTAAGTTTCGGTCCATCATCGCACTCTTTTTCGTGCTCTGTCTCTTTTTCCTGCT	75
Db	1	MetAlaLysPheValSerIleIleThrLeuPhePheAlaAlaLeuValLeuPheAlaAla	20
Qy	76	TTTGAAGCACCACATGTTGGAAGCACAGAGTTGTGGAAAGGCCCAAGTGGACATGG	135
Db	21	PheGluAlaProThrMetValLysAlaGlnLysLeuCysGluArgSerSerGlyThrTyr	40
Qy	136	TCAGGAGTCTGTGGAAACAATAACCATCGCAGAGATCATAGTCAGTTAACTTCGAAAGCA	195
Db	41	SerGlyValCysGlyAsnAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla	60
Qy	196	CGACATGGATCTTGCAACTATGCTTTCCAGCTCACAAGTCTATCTGCTACTTTCCTTGT	255

Db 61 ArgHisGlySerCysAsnTyrValPheProTyrHisArgCysIleCysTyrPheProCys 80
 RESULT 4
 Q9F122
 ID Q9F122 PRELIMINARY; PRT; 80 AA.
 AC Q9F122
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Antifungal protein-like.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cv. Columbia;
 RX MEDLINE=99397451; PubMed=10470850;
 RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
 RA Miyajima N., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.
 RT Sequence features of the regions of 1,011,550 bp covered by seventeen
 RT P1 and TAC clones";
 RL DNA Res. 6:183-195(1999).
 DR EMBL; AB017085; BAB09150.1; -;
 DR HSPF; P30231; IAYJ.
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro; IPR008176; Gamma-thionin.
 DR InterPro; IPR003614; Knot1.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G-Purothionin; 1.
 DR SMART; SM00505; Knot1; 1.
 DR PROSITE; PS00940; GAMMA THIONIN; 1.
 SQ SEQUENCE 80 AA; 8550 MW; 44ELF6D8452AC76E CRC64;
 Alignment Scores:
 Pred. No.: 3,01e-38 Length: 80
 Score: 398.00 Matches: 71
 Percent Similarity: 93.75% Conservative: 4
 Best Local Similarity: 88.75% Mismatches: 5
 Query Watch: 52.93% Indels: 0
 DB: 10 Gaps: 0
 US-10-006-252a-19 (1-414) x Q9F122 (1-80)
 QY 16 ATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGTGCTGCTCTTTTGTCTGCT 75
 Db 1 MetAlaLysSerAlaThrIleThrPheLeuPheAlaLeuValLeuPheAlaAla 20
 QY 76 TTGGAAGCACCACATGTTGGAGACACAGAGTTGTGGAAGCCAGGCGGACATGG 135
 Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAACAATAACGCATGCAGATCATGCTTACCTTGCAGAAACA 195
 Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
 QY 196 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTATGCTACTTCTTCTGT 255
 Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80
 RESULT 5
 Q9F231
 ID Q9F231 PRELIMINARY; PRT; 80 AA.
 AC Q9F231
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative antifungal protein (Cysteine-rich antifungal protein,
 DE putative).
 GN T24C10.12 OR F14C21.57.
 OS Arabidopsis thaliana (Mouse-ear cress).
 Db 61 ArgHisGlySerCysAsnTyrValPheProTyrHisArgCysIleCysTyrPheProCys 80
 RESULT 4
 Q9F122
 ID Q9F122 PRELIMINARY; PRT; 80 AA.
 AC Q9F122
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Antifungal protein-like.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cv. Columbia;
 RX MEDLINE=99397451; PubMed=10470850;
 RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
 RA Miyajima N., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.
 RT Sequence features of the regions of 1,011,550 bp covered by seventeen
 RT P1 and TAC clones";
 RL DNA Res. 6:183-195(1999).
 DR EMBL; AB017085; BAB09150.1; -;
 DR HSPF; P30231; IAYJ.
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro; IPR008176; Gamma-thionin.
 DR InterPro; IPR003614; Knot1.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G-Purothionin; 1.
 DR SMART; SM00505; Knot1; 1.
 DR PROSITE; PS00940; GAMMA THIONIN; 1.
 SQ SEQUENCE 80 AA; 8550 MW; 44ELF6D8452AC76E CRC64;
 Alignment Scores:
 Pred. No.: 3,01e-38 Length: 80
 Score: 398.00 Matches: 71
 Percent Similarity: 93.75% Conservative: 4
 Best Local Similarity: 88.75% Mismatches: 5
 Query Watch: 52.93% Indels: 0
 DB: 10 Gaps: 0
 US-10-006-252a-19 (1-414) x Q9F122 (1-80)
 QY 16 ATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGTGCTGCTCTTTTGTCTGCT 75
 Db 1 MetAlaLysSerAlaThrIleThrPheLeuPheAlaLeuValLeuPheAlaAla 20
 QY 76 TTGGAAGCACCACATGTTGGAGACACAGAGTTGTGGAAGCCAGGCGGACATGG 135
 Db 21 PheGluAlaProThrMetValGluAlaGlnLysLeuCysGluLysProSerGlyThrTrp 40
 QY 136 TCAGGAGTCTGTGGAACAATAACGCATGCAGATCATGCTTACCTTGCAGAAACA 195
 Db 41 SerGlyValCysGlyAsnSerAsnAlaCysLysAsnGlnCysIleAsnLeuGluGlyAla 60
 QY 196 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTATGCTACTTCTTCTGT 255
 Db 61 LysHisGlySerCysAsnTyrValPheProAlaHisLysCysIleCysTyrValProCys 80
 RESULT 5
 Q9F231
 ID Q9F231 PRELIMINARY; PRT; 80 AA.
 AC Q9F231
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative antifungal protein (Cysteine-rich antifungal protein,
 DE putative).
 GN T24C10.12 OR F14C21.57.
 OS Arabidopsis thaliana (Mouse-ear cress).
 Db 61 ArgHisGlySerCysAsnTyrValPheProTyrHisArgCysIleCysTyrPheProCys 80
 RESULT 4
 Q9F122
 ID Q9F122 PRELIMINARY; PRT; 80 AA.
 AC Q9F122
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Antifungal protein-like.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cv. Columbia;
 RX MEDLINE=99397451; PubMed=10470850;
 RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
 RA Miyajima N., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX.
 RT Sequence features of the regions of 1,011,550 bp covered by seventeen
 RT P1 and TAC clones";
 RL DNA Res. 6:183-195(1999).
 DR EMBL; AB017085; BAB09150.1; -;
 DR HSPF; P30231; IAYJ.
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro; IPR008176; Gamma-thionin.
 DR InterPro; IPR003614; Knot1.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G-Purothionin; 1.
 DR SMART; SM00505; Knot1; 1.
 DR PROSITE; PS00940; GAMMA THIONIN; 1.
 SQ SEQUENCE 80 AA; 8550 MW; 44ELF6D8452AC76E CRC64;
 Alignment Scores:
 Pred. No.: 1.4e-15 Length: 80
 Score: 207.00 Matches: 40
 Percent Similarity: 67.90% Conservative: 15
 Best Local Similarity: 49.38% Mismatches: 24
 Query Watch: 27.53% Indels: 2
 DB: 10 Gaps: 2
 US-10-006-252a-19 (1-414) x Q9F231 (1-80)
 QY 16 ATGGCTAAGTTTGGTCCATCATCGCACTCTTTTGTGCTGCTCTTTTGTCTGCT 75
 Db 1 MetAlaLysPheCysThrThrIleThrLeuIleLeuValAlaLeuValPheAlaAsp 20
 QY 76 TTGGAAGCACCACATGTTGGAGACACAGAGTTGTGGAAGCCAGGCGGACATGG 135
 Db 21 PheGluAlaProThrIleValLysAlaGlu--LeuCysLysArgGluSerGluThrTrp 39
 QY 136 TCAGGAGTCTGTGGAACAATAACGCATGCAGATCATGCTTACCTTGCAGAAACA 195
 Db 40 SerGlyArgCysValAsnAspThrGlnCysArgAspHisCysIleAsnAspArgGly 59
 QY 196 CGACATGGATCTTGCACATATGCTTCCAGCTCACAAGTATGCTACTTCTTCTGT 252
 Db 60 AsnAspGlyTyrCysAlaGlyGlyTyrProThrTyrArgSerCysPhePheSer 79

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Qy	253 TGT 255 80 Cys 80
Db	
RESULT 6	
Q8VZQ7	PRELIMINARY; PRT; 78 AA.
ID	Q8VZQ7
AC	Q8VZQ7
DT	01-MAR-2002 (TrEMBLrel. 20, Created)
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Putative defensin AMP1 protein.
GN	AT1G19610.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.
NCBI_TaxID=3702;	
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Federspiel N.A., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
RA	Yamada K., Banj J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA	Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA	Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA	Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA	Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA	Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA	Shinn P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
RA	Theologis A.;
RT	"Full length cDNA of gene At1g19610 (GI:15223595).";
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Yamada K., Banj J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA	Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA	Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA	Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA	Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA	Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA	Shinn P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
RA	Theologis A.;
RT	"Arabidopsis Open Reading Frame (ORF) Clones";
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN	EMBL; AY063933; AAL36289.1; -
DR	InterPro; IPR008176; Gamma-thionin.
DR	Pfam; PF00304; Gamma-thionin; 1.
DR	ProDom; PD002594; G-Purothionin; 1.
DR	PROSITE; PS00940; GAMMA THIONIN; 1.
SQ	SEQUENCE 78 AA; 8840 MW; ASBDD28303A6545 CRC64;
Alignment Scores:	
Pred. No.:	1.7e-12 Length: 78
Score:	181.00 Matches: 31
Percent Similarity:	53.95% Conservative: 10
Best Local Similarity:	40.79% Mismatches: 35
Query Match:	24.07% Indels: 0
DB:	Gaps: 0
US-10-006-252A-19 (1-414) x Q8VZQ7 (1-78)	
Qy	28 GGTCATCATCGCACTTTTTCCTGCTCTTTTTCCTTTTTCCTGCTTTTTCCTGCAAGCACC 87
Db	3 SerSerTyThrLeuMetLeuPheLeuCysLeuSerIlePheLeuAlaSerThrGlu 22
Qy	88 ACATGGTGGAAGCACAGACTTGTGCAGAACGACGAGTGGGACGATGCGATGCTCT 147
Db	23 McMetAlaValGLuglyArgilecysgluargSerlysThrTrpThrGlyPheCys 42
Qy	148 GGAACAATAAGCAGTAAGTAACTTGCATTAACTTGCAGAACGACGATGATCT 207
Db	43 GlyAsnThrArgGlyCysAspSerGlnCysylsArgTrpGluArgAlaSerHisGlyAla 62

[illegible]

Best Local Similarity: 38.64% Mismatches: 25
 Query Match: 18.55% Indels: 19
 DB: 10 Gaps: 5

US-10-006-252A-19 (1-414) x Q84ZX5 (1-132)

QY 16 ATGCTAAGTTTGGCTCCATC---GCACTCTTTTTCGCTCTTGTCTTTTCT 72
 Db 1 MetAlaLysCysSerTyrValPheCysAlaValLeuLeuPheLeuValAlaIleGly 20
 QY 73 GCYTTCGAACCAACAAATGGTGGAGCACAGAGTTGTGGAAAGCCCAAGTGGACA 132
 Db 21 GluMetGluAla-----AlaGlySerLysLeuCysGluLysThrSerLysThr 36
 QY 133 TGGTCAGAGCTCTGTGGAACAAATAACGCAATCAAGTCAAGTCAAGTCAAGTCAAG 192
 Db 37 TyrSerGlyLysCys---AspAsnLysLysCysAspLysLysCysIleGluTrpGluLys 55
 QY 193 GCAGCATGATCTTGCACACTATGCTTCCAGCTCAACAG----- 234
 Db 56 AlaGlnHisGlyAlaCys-----HisLysArgGluAlaGlyLysGlu 69
 QY 235 ---TGTATCTGCTACTTCTCTCT 255
 Db 70 SerCysPheCysTyrPheAspCys 77

RESULT 11

Q8GTM2 ID Q8GTM2 PRELIMINARY; PRT; 83 AA.
 AC Q8GTM2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative plant defensin SPIIB.
 OS Picea abies (Norway spruce) (Picea excelsa).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
 OX NCBI_TaxID=3329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Needle;
 RA Fossdal C.G.;
 RT "The putative gymnosperm plant defensin (SPII) accumulates after seed
 RT germination and a related SPIIB cDNA is found in needles.";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF548021; AAN40688.1; -;
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro; IPR008176; Gamma-thionin.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G Purothionin; 1.
 DR SMART; SM00505; Knott1; 1.
 DR PROSITE; PS00940; GAMMA_THIONIN; 1.
 SQ SEQUENCE 83 AA; 888 MW; E45BF9E61B9AA3D2 CRC64;

Alignment Scores:
 Pred. No.: 5,14e-05 Length: 83
 Score: 118.00 Matches: 26
 Percent Similarity: 51.32% Conservative: 13
 Best Local Similarity: 34.21% Mismatches: 35
 Query Match: 15.69% Indels: 2
 DB: 10 Gaps: 2

US-10-006-252A-19 (1-414) x Q8GTM2 (1-83)

QY 31 TCACATATCGCACTCTTTTTCGCTCTTGTCTTTTTCGCTTTTTCGACCAACA 90
 Db 8 SerArgLeuSerAlaLeuPheLeuValLeuValLeuValLeuValLeuValLeuVal 27
 QY 91 ATGGTGGAGCAAG---AAGTTGTGCGAAGCCCAAGTGGGACATGGTCAGAGTCTGT 147
 Db 28 LeuLuprolaGluGlyArgThrCysLysThrProSerGlyLysPheLysGlyValCys 47

QY 148 GGAAACAATAACGCAATGCAAGATCAGTGCATTAACTTGAGAAAGCACGACATGGATCT 207
 Db 48 AlaSerArgAsnAsnCysLysAsnValCys---GlnThrGluGlyPheProSerGlySer 66
 QY 208 TGCACACTATCTCTCCAGCTCACAGTGTATCTGCTACTTTCCTCTGT 255
 Db 67 CysAspPheHisValAlaAsnArgLysCysTyrCysSerLysProCys 82

RESULT 12

Q8GTM0 ID Q8GTM0 PRELIMINARY; PRT; 105 AA.
 AC Q8GTM0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Flower-specific defensin precursor.
 GN NAD1.
 OS Nicotiana glauca (Winged tobacco) (Persian tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4087;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lay F.T., Schirra H.J., Scanlon M.J., Anderson M.A., Craik D.J.;
 RT "The three-dimensional solution structure of NAD1, a new floral
 RT defensin from Nicotiana glauca and its application to a homology model
 RT of the crop defense protein alfAFP.";
 RL J. Mol. Biol. 0:0-0(2003).
 DR EMBL; AF509566; AAN70999.1; -;
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro; IPR008176; Gamma-thionin.
 DR Pfam; PF00304; Gamma-thionin; 1.
 DR ProDom; PD002594; G Purothionin; 1.
 DR SMART; SM00505; Knott1; 1.
 DR PROSITE; PS00940; GAMMA_THIONIN; 1.
 FT CHAIN 26 72 FLOWER-SPECIFIC DEFENSIN.
 SQ SEQUENCE 105 AA; 11722 MW; DA7F41736CEB5A33 CRC64;

Alignment Scores:
 Pred. No.: 9,01e-05 Length: 105
 Score: 116.00 Matches: 27
 Percent Similarity: 53.66% Conservative: 17
 Best Local Similarity: 32.93% Mismatches: 30
 Query Match: 15.43% Indels: 8
 DB: 10 Gaps: 4

US-10-006-252A-19 (1-414) x Q8GTM0 (1-105)

QY 16 ATGGCTAAGTTTGGCTCCATCAGCACTCTTTTTCGCTCTTGTCTTTTTCGCTGT 75
 Db 1 MetAlaArgSerLeuCysPheMetAlaPheAlaLeuAlaMetMetLeuPheValAla 20
 QY 76 TTCGAAGCACCAACAATGGTGAAGCACAGAGTTGTGCGAAGCCCAAGTGGGACATGG 135
 Db 21 TyrGlu-----ValGlnAlaArgGlu---CysLysThrGluSerAsnThrPhe 35
 QY 136 TCAGGAGTCTGTGGAACAATAACGCAATCAGTCAAGATCAGTTCATTAACCTTGAGAAAGCA 195
 Db 36 ProGlyIleCysIleThrLysProCysArgLysAlaCysIleSer---GluLysPhe 54
 QY 196 CGACATGATCTTGCACACTATGCTTCCAGCTCACAGTGTATCTGCTACTTTCCTTGT 255
 Db 55 ThrAspGlyHisCysSerLysIleLeu-----ArgArgCysLeuCysThrLysProCys 72
 QY 256 TAATTT 261
 Db 73 ValPhe 74
 RESULT 13
 Q40779 PRELIMINARY; PRT; 83 AA.
 ID Q40779

DR InterPro; IPR003614; Knot1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; G Purothionin; 1.
DR SMART; SM00505; Knot1; 1.

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:

US-10-006-252A-19 (1-414) x Q8W434 (1-75)

Qy	31	TCATCATCGCACTCTCTTTTGGCTGCTCTGTTTCTCTTTTGGCTGCTCTTCGAGCACCACAA	90
Db	5	SerLeuAlaGlyLeuCysPheLeuPheValLeuPheValAlaGlnGluValMetVal	24
Qy	91	ATGTGGGAAGCACACAAGTTGTGGAAAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGA	150
Db	25	GlnThrGluAla---LysThrCysGluAsnLeuAlaAsnThrTyrArgGlyProCysPhe	43
Qy	151	AACAATAAGCATGCAGGAATCAGTGCATTAACTTCGAGAAAGCACGACATGGATCTTGC	210
Db	44	ThrThrGlySerCysAspAspHisCysIysAsnIysGluHisLeuArgSerGlyArgCys	63
Qy	211	AACATATGCTTCCGAGCTCACAAAGTATATCTGCTACTTCTCTGT	255
Db	64	ArgAspAspPhe-----ArgCysTrpCysThrArgAsnCys	75

Search completed: May 11, 2004, 17:04:29
Job time : 43 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 08:49:06 ; Search time 1784 Seconds
(without alignments)
10058.305 Million cell updates/sec

Title: US-10-006-252A-19

Perfect score: 414

Sequence: 1 gttttattagatcatggc.....caaaaaaaaaaaaaaaaaaaaaa 414*

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_hg.*

3: gb_in.*

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6: gb_pat.*

7: gb_ph.*

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14: gb_vi.*

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16: em_fun.*

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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	414	100.0	414	6	A26875 R.sativus A
2	414	100.0	414	6	A39549 Sequence 37
3	414	100.0	414	6	A63404 Sequence 19
4	414	100.0	414	6	AR050153 Sequence
5	414	100.0	414	6	AR130272 Sequence
6	414	100.0	414	6	AR130272 Sequence 48
7	414	100.0	414	6	AR207337 Sequence
8	414	100.0	414	6	AR374914 Sequence
9	394	95.2	395	8	RSU18557
10	255	61.6	449	6	E34290
11	254.2	61.4	288	6	A39553 Sequence 41
12	254.2	61.4	288	6	AR050161 Sequence
13	254.2	61.4	288	6	AR130280 Sequence
14	254.2	61.4	288	6	I23736 Sequence 58
15	249.8	60.3	457	8	RSU18556
16	242.4	58.6	403	6	A68645 Sequence 13
17	242.4	58.6	403	8	ATANTSPEC
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19	232.4	56.1	575	6	BD232249 Method of
20	229	55.3	454	8	AY063779 Arabidops
21	223	53.9	400	6	A68647 Sequence 15
22	219	52.9	285	6	AR014692 Sequence
23	219	52.9	285	6	AR432392 Sequence
24	215.8	52.1	285	6	AR014693 Sequence
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26	212.2	51.2	451	8	ENU59459 Brassica na
27	210.4	50.8	475	8	RSEFF3
28	207	50.0	499	8	RSAPF4
29	206	49.8	363	8	AF528180
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ALIGNMENTS

RESULT 1	A26875	R.sativus	APPI	Gene.	414 bp	DNA	linear	PAT 30-NOV-2001
LOCUS	A26875	R.sativus	APPI	Gene.				
DEFINITION	A26875	R.sativus	APPI	Gene.				
ACCESSION	A26875	R.sativus	APPI	Gene.				
VERSION	A26875.1	GI:1247352						
KEYWORDS		Raphanus sativus (radish)						
SOURCE		Raphanus sativus						
ORGANISM		Raphanus sativus						
REFERENCE		1. (bases 1 to 414)						
AUTHORS		Broekaert, W.F., Cammue, B.P.A., Terras, F.R.G., Vanderleyden, J., Osborn, R.W. and Rees, S.B.						

TITLE BIOCIDAL PROTEINS
JOURNAL Patent: WO 9305153-A 33 18-MAR-1993;
ICI PLC (GB)
FEATURES Location/Qualifiers
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/organism="Raphanus sativus"
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Best Local Similarity 100.0%; Pred. No. 5e-88;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

LOCUS A39549 414 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 37 from Patent WO9416076.
ACCESSION A39549
VERSION A39549.1 GI:2295842

SOURCE
unidentified
unclassified.

REFERENCE 1 (bases 1 to 414)
AUTHORS Dubock,A.C., Powell,K.A. and Rees,S.B.
TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
JOURNAL Patent: WO 9416076-A 37 21-JUL-1994;
ZENECA LTD (GB)

COMMENT Other publication AU 5820494 940815.
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5e-88;
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RESULT 3

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DEFINITION Sequence 19 from Patent WO9721814.
ACCESSION A63404

VERSION A63404.1 GI:3717176
KEYWORDS
unidentified
unclassified.

ORGANISM
unidentified
unclassified.

REFERENCE 1
AUTHORS Broekaert,W.F., De,S.G., Rees and Sarah,B.
TITLE ANTI-FUNGAL PROTEINS
JOURNAL Patent: WO 9721814-A 19 19-JUN-1997;
ZENECA LTD (GB)
COMMENT Other publication AU 1105397 19970703.
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5e-88;
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LOCUS AR050153 414 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 48 from patent US 5824869.
ACCESSION AR050153
VERSION AR050153.1 GI:5972145
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 414)
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
Terras,F.R.G. and Vanderleyden,J.
TITLE Biocidal proteins
JOURNAL
PATENT: US 5824869-A 48 20-OCT-1998;
LOCATION/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5e-88;
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LOCUS AR130272 414 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 48 from patent US 6187904.
ACCESSION AR130272
VERSION AR130272.1 GI:14118169
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 414)
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
Terras,F.R.G. and Vanderleyden,J.
TITLE Biocidal proteins
JOURNAL
PATENT: US 6187904-A 48 13-FEB-2001;
LOCATION/Qualifiers
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DEFINITION Sequence 48 from patent US 5538525.
ACCESSION AR130278
VERSION AR130278.1 GI:1603598
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 414)
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
Terras,F.R.G. and Vanderleyden,J.
TITLE Biocidal proteins
JOURNAL
PATENT: US 5538525-A 48 23-JUL-1996;
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RESULT 7
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 DEFINITION Sequence 19 from patent US 6372888.
 ACCESSION AR207337
 VERSION AR207337.1 GI:21506219
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 414)
 AUTHORS De Samblanx, G. W. J., Broekaert, W. Frans., and Rees, S. Bronwen.
 TITLE Antifungal proteins
 JOURNAL Patent: US 6372888-A 19 16-APR-2002;
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 DEFINITION Sequence 45 from patent US 6605698.
 ACCESSION AR374914
 VERSION AR374914.1 GI:40077932
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 414)
 AUTHORS Van Amerongen, A., Fant, F., Borremans, F. A., De Samblanx, G. W., Sijtsma, L., Melen, R. H., Puijk, W. C., Schaaper, W. M. M., Broekaert, W. F., van Gelder, W. M. J., and Rees, S. B.
 TITLE Antifungal peptides and composition thereof
 JOURNAL Patent: US 6605698-A 45 12-AUG-2003;
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 Location/Qualifiers
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 Best Local Similarity 100.0%; Pred. No. 5e-88;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 361 GTTGGTTCGGTTATACAAATAAGTTTATTCACCAAAAAAAAAAAAAAAAAAAAA 414

RESULT 9
 RSU18557
 LOCUS 395 bp mRNA linear PLN 07-JUL-1995
 DEFINITION Raphanus sativus antifungal protein 1 preprotein (Rs-AP1) mRNA,
 complete cds.
 ACCESSION U18557
 VERSION U18557.1 GI:644773
 KEYWORDS Raphanus sativus (radish)
 SOURCE Raphanus sativus
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.

```

REFERENCE
AUTHORS
  Terras,F.R.G., Eggermont,K., Kovaleva,V., Raikhel,N.V.,
  Osborn,R.W., Kester,A., Rees,S.B., Torrekens,S., Van Leuven,F.,
  Vanderleyden,J., Cammue,B.P.A. and Broekaert,W.F.
TITLE
  Small cysteine-rich antifungal proteins from radish: their role in
  host defense
JOURNAL
  Plant Cell 7, 568-573 (1995)
AUTHORS
  Terras,F.R.
TITLE
  Direct Submission
COMMENT
  Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
  of Genetics, Applied Biological Sciences, W. De Croylaan 42,
  Heverlee, Belgium, B-3001
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      /evidence=experimental
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  DB  62  TCTTTTGTGCTTTCCGAGCACCACCAATGTTGGAAGCACAGAGTTGTGGAAGGCC 121
  QY  123  AAGTGGACATGTCAGGAGTCTGTGGAACCAATACCGATCGAAGATCGATCAATAA 182
  DB  122  AAGTGGACATGTCAGGAGTCTGTGGAACCAATACCGATCGAAGATCGATCAATAA 181
  QY  183  CCTTGAGAAAGCAGCATGGATCTTGCACATATGTCTTCCAGCTCACAAGTGTATCTG 242
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  QY  243  CTACTTCCTTGTAAATTTATCGCAACTCTTTGGTGAATAGTTTTATGTAATTACAC 302
  DB  242  CTACTTCCTTGTAAATTTATCGCAACTCTTTGGTGAATAGTTTTATGTAATTACAC 301

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DB   362  TGGTTCGGTTATACAAATAAAGTTTATTTCACCA 395

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Phage and plasmid constructed by ligating antibacterial protein
gene DNA with vector DNA, transformant microorganism and
transformant plant containing the same and antibacterial protein.
E34290      GI:18624295
KEYWORDS    JP 2000116379-A/1.
SOURCE      unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 449)
AUTHORS      Shoji,K.
TITLE        Phage and plasmid constructed by ligating antibacterial protein
              gene DNA with vector DNA, transformant microorganism and
              transformant plant containing the same and antibacterial protein
JOURNAL      Patent: JP 2000116379-A 1 25-APR-2000;
              TOYAMA PREF
COMMENT      OS Raphanus sativus L.
              PN JP 2000116379-A/1
              PD 25-APR-2000
              PF 09-OCT-1998 JP 1998288472
              PR KAZUAKI SHOJI
              PI C12N15/09,A01H5/00,A01N65/00,C07K14/415,C12N1/21,C12N5/10// PC
              (C12N15/09,C12R1:91),(C12N1/21,C12R1:19),(C12N5/10,C12R1:91), PC
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              PC C12N5/00,(C12N15/00,C12R1:91),(C12N5/00,C12R1:91) CC
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              FT source 1..449
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    Best Local Similarity 81.0%; Pred. No. 3e-50;
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  QY  4  TTATTAGTCATCGCTAAGTTTCGTCCTCATCGCACTCTTTTGTGCTCTGT 63
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  QY  64  CTTTGTGCTGCTTTCCGAGCACCACCAATGTTGGAAGCACAGAGTTGTGGAAGGCCA 123
  DB  89  GTTTTTCGCTTTCCGAGCACCACCAATGTTGGAAGCACAGAGTTGTGGAAGGCCA 148
  QY  124  AGTGGACATGTCAGGAGTCTGTGGAACCAATACCGATCGAAGATCGATCAATAA 183
  DB  149  AGTGGACATGTCAGGAGTCTGTGGAACCAATACCGATCGAAGATCGATCAATAA 208
  QY  184  CTTTGAGAAAGCAGCATGGATCTTGCACATATGTCTTCCAGCTCACAAGTGTATCTGC 243
  DB  209  CTTTGAGAAAGCAGCATGGGCTTGTGCAACTATGTCTTCCAGCTCACAAGTGTATCTGT 268
  QY  244  TACTTTCCTTGTAAATTTATCGCAACTCTTTGGTGAATAGTTT--TTATGTAATTAC 300
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QY 360 TGTGTTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAA 410
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RESULT 11
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LOCUS A39553 288 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 41 from Patent WO9416076.
ACCESSION A39553
VERSION A39553.1 GI:2295844
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 288)
AUTHORS Dubock,A.C., Powell,K.A. and Rees,S.B.
TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
JOURNAL Patent: WO 9416076-A 41 21-JUL-1994;
ZENECA LTD (GB)
COMMENT Other publication AU 5820494 940815.
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Best Local Similarity 98.8%; Pred. No. 4.9e-50;
Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 60
Db 28 GTTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 87

QY 61 GTTCTTTTGTCTGCTTTCGAAGCACCACCAATGGTGGAGACACAGAGTTGTGCGAAGG 120
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QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 180
Db 148 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 207

QY 181 AACCTTGAGAAAGCAGACATGGATCTTGGAACTATGTCTTCCAGCTCACAAGTGTATC 240
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QY 241 TGCTACTTTCCTTGTAAAT 259
Db 268 TGCTACTTTCCTTGTAAAT 286

RESULT 12
A39553
LOCUS A39553 288 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 58 from patent US 5824869.
ACCESSION A39553
VERSION A39553.1 GI:5972153
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 288)
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
Terras,F.R.G. and Vanderleyden,J.
TITLE Biocidal proteins
JOURNAL Patent: US 5824869-A 58 20-OCT-1998;
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ORIGIN
Query Match 61.4%; Score 254.2; DB 6; Length 288;
Best Local Similarity 98.8%; Pred. No. 4.9e-50;
Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 60
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QY 61 GTTCTTTTGTCTGCTTTCGAAGCACCACCAATGGTGGAGACACAGAGTTGTGCGAAGG 120
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QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 180
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Best Local Similarity 98.8%; Pred. No. 4.9e-50;
Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 60
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QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 180
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QY 181 AACCTTGAGAAAGCAGACATGGATCTTGGAACTATGTCTTCCAGCTCACAAGTGTATC 240
Db 208 AGACTTGAGAAAGCAGACATGGATCTTGGAACTATGTCTTCCAGCTCACAAGTGTATC 267

QY 241 TGCTACTTTCCTTGTAAAT 259
Db 268 TGCTACTTTCCTTGTAAAT 286

RESULT 13
AR130280
LOCUS AR130280 288 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 58 from patent US 6187904.
ACCESSION AR130280
VERSION AR130280.1 GI:14118177
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 288)
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
Terras,F.R.G. and Vanderleyden,J.
TITLE Biocidal proteins
JOURNAL Patent: US 6187904-A 58 13-FEB-2001;
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Best Local Similarity 98.8%; Pred. No. 4.9e-50;
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QY 1 GTTTTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 60
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QY 61 GTTCTTTTGTCTGCTTTCGAAGCACCACCAATGGTGGAGACACAGAGTTGTGCGAAGG 120
Db 88 GTTCTTTTGTCTGCTTTCGAAGCACCACCAATGGTGGAGACACAGAGTTGTGCGAAGG 147

QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 180
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QY 181 AACCTTGAGAAAGCAGACATGGATCTTGGAACTATGTCTTCCAGCTCACAAGTGTATC 240
Db 208 AGACTTGAGAAAGCAGACATGGATCTTGGAACTATGTCTTCCAGCTCACAAGTGTATC 267

QY 241 TGCTACTTTCCTTGTAAAT 259
Db 268 TGCTACTTTCCTTGTAAAT 286
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Db      268 TGCTACTTCCCTGTTAAAT 286

RESULT 14
I23736
LOCUS      I23736                      288 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION Sequence 58 from patent US 5538525.
ACCESSION  I23736
VERSION     I23736.1  GI:1603606
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 288)
AUTHORS    Broekaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
            Terras, F.R.G. and Vanderleyden, J.
TITLE      Biocidal proteins
JOURNAL    Patent: US 5538525-A 58 23-JUL-1996;
FEATURES   Location/Qualifiers
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Best Local Similarity 98.8%; Pred. No. 4.9e-50;
Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GTTTATTAGTATGATGGCTAAGTTGGCTCCATCATCGCACTTCTTTTCTGCTCTT 60
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QY      61 GTTCTTTTCTGTTTCGAAGCACCACAAATGGTGGAGCAGACAGAGTTGCGAAAGG 120
Db      88 GTTCTTTTCTGTTTCGAAGCACCACAAATGGTGGAGCAGACAGAGTTGCGAAAGG 147
QY      121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAAGCATGCAAGATCAGTGCATT 180
Db      148 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAAGCATGCAAGATCAGTGCATT 207
QY      181 AACCTTGAGAAAGCAGACATGATGCTTGCACATGCTTCCAGCTCACAAGTGTATC 240
Db      208 AGACTTGAGAAAGCAGACATGATGCTTGCACATGCTTCCAGCTCACAAGTGTATC 267
QY      241 TGCTACTTTCCTGTTAAAT 259
Db      268 TGCTACTTTCCTGTTAAAT 286

RESULT 15
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LOCUS      RSU18556                      457 bp      mRNA      linear      PLN 07-JUL-1995
DEFINITION Raphanus sativus antifungal protein 2 preprotein (Rs-APP2) mRNA,
            complete cds.
ACCESSION  U18556
VERSION     U18556.1  GI:609319
KEYWORDS
SOURCE      Raphanus sativus (radish)
ORGANISM    Raphanus sativus
REFERENCE   1 (sites)
AUTHORS    Terras, F.R.G., Eggermont, K., Kovaleva, V., Raikhel, N.V.,
            Osborn, R.W., Kester, A., Rees, S.B., Torrekens, S., Van Leuven, F.,
            Vanderleyden, J., Cammue, B.P.A. and Broekaert, W.F.
TITLE      Small cysteine-rich antifungal proteins from radish: their role in
            host defense
JOURNAL    Plant Cell 7, 568-573 (1995)
REFERENCE   2 (bases 1 to 457)
AUTHORS    Terras, F.R.
TITLE      Direct Submission
JOURNAL    Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory

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of Genetics, Applied Biological Sciences, W. De Croylaan 42,
Heverlee, Belgium, B-3001
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                        /function="antifungal, fungistatic"
                        /note="Evidence for antifungal activity: Analysis of two
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Query Match      60.3%; Score 249.8; DB 8; Length 457;
Best Local Similarity 80.4%; Pred. No. 5.1e-49;
Matches 329; Conservative 0; Mismatches 76; Indels 4; Gaps 3;

QY      4 TTATTAGTATGATGCTAAGTTGGCTCCATCATCGCACTTCTTTTCTGCTCTTGT 63
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QY      64 CTTTTCCTGCTTTCGAGCACCACAAATGGTGGAGCAGACAGAGTTGCGAAGGCCA 123
Db      90 GTTTTTCCTGCTTTCGAGCACCACAAATGGTGGAGCAGACAGAGTTGCGAAGGCCA 149
QY      124 AGTGGACATGCTCAGGAGTCTGTGAAACAAATAACGCATGCAAGAATCAGTGCATTAA 183
Db      150 AGTGGACATGCTCAGGAGTCTGTGAAATAATAACGCATGCAAGAATCAGTGCATTGA 209
QY      184 CTTGAGAAAGCAGCATGGATCTTGGCAACTATGCTTCCAGCTCACAAGTGTATCTGC 243
Db      210 CTTGAGAAAGCAGCATGGGCTTTCGAATATGCTTCCAGCTCACAAGTGTATCTGT 269
QY      244 TACTTTCCTGTTTAATTTATCGCAAACTCTTTGGTGAATAGTTT--TTATGTAATTTAC 300
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QY      301 ACAAAATAAGTCAGTGTCTACTATCCATGAGTGAATTTTAAGACATGTACCAGATATG-TTA 359
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QY      360 TGTGTGTTGGTTATACAAATAAAGTTTATTACCAAAAAA 408
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	414	100.0	414	2	AAQ72333
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5	223.8	78.2	394	9	ADCS1221
6	307.8	74.3	426	9	ADCS1223
7	255	61.6	449	3	AAAS3190
8	254.2	61.4	261	2	AAQ38652
9	254.2	61.4	288	2	AAQ70130
10	242.4	58.6	403	2	AAV10632
11	232.4	56.1	575	3	AAZ99339
12	223	53.9	400	2	AAV10633
13	203.4	49.1	500	2	AAQ94581
14	202.6	48.9	414	3	AAZ39123
15	201	48.6	416	3	AAZ39124
16	199.8	48.3	243	6	ABQ82690
17	199.8	48.3	243	7	ADA68378
18	198.2	47.9	243	6	ABQ82691
19	196.6	47.5	243	6	ABZ14241
20	196.6	47.5	243	7	ABZ42136
21	194.6	47.0	308	2	AAQ94577
22	193.8	46.8	481	2	AAQ99289
23	180	43.5	270	2	AAQ94582

ALIGNMENTS

RESULT 1

AAQ38650	286	2	AAQ94574
ID	AAQ38650 standard; DNA; 414 BP.		
XX	AAQ38650;		
AC	AAQ38650;		
XX	25-MAR-2003 (revised)		
DT	07-JUL-1993 (first entry)		
XX	RS-AFP1 cDNA.		
XX	Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;		
KW	fungicide; bactericide; antibiotic; antifungal; gram positive;		
KW	plant disease resistance; low toxicity.		
XX	Raphanus sativus.		
OS	Raphanus sativus.		
PH	Key		
FT	CDS		
FT	Location/Qualifiers		
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XX	WO9305153-Al.		
XX	18-MAR-1993.		
PD	27-AUG-1992; 92WO-GB001570.		
XX	29-AUG-1991; 91GB-00018523.		
PR	13-FEB-1992; 92GB-00003038.		
PR	25-JUN-1992; 92GB-00013526.		
XX	(ICIL) IMPERIAL CHEM IND PLC.		
PA	Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;		
XX	Vanderleyden J;		
PI	WPI; 1993-100978/12.		
PI	Biocidal proteins isolated from seeds of plants - e.g. brassica or		
DR	danlia, useful for increasing plants' resistance to fungal and bacterial		
XX	diseases.		
XX	Example 21; Fig 35; 110pp; English.		
XX	This cDNA represents the sequence of Rs-AFP1 from Raphanus sativus. PCR		
CC	primer AAQ38640 was used together with AAQ38641 to generate a probe for		

24	178.8	43.2	286	2	AAQ94574
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33	147.6	35.7	443	3	AAQ99330
34	145.8	35.2	485	3	AAQ99337
35	145.8	35.2	1093	3	AAQ99334
36	145.4	35.1	437	3	AAQ99331
37	145	35.0	434	3	AAQ99332
38	144.6	34.9	488	3	AAQ99338
39	144.2	34.8	446	3	AAQ99329
40	144.2	34.8	485	3	AAQ99335
41	144.2	34.8	557	3	AAQ99336
42	129.8	31.4	284	2	AAQ38651
43	129.8	31.4	284	2	AAQ70129
44	104.2	25.2	306	2	AAQ94580
45	74.6	18.0	243	9	ADC87758

Aac94574 Alyssum s
Aac46924 Arabidops
Aac99324 DNA encod
Aac99327 DNA encod
Aac99326 DNA encod
Aac10646 A. thalia
Aac51396 Portion o
Aac99325 DNA encod
Aac99333 DNA encod
Aac99330 DNA encod
Aac99337 DNA encod
Aac99334 DNA encod
Aac99331 DNA encod
Aac99332 DNA encod
Aac99338 DNA encod
Aac99329 DNA encod
Aac99335 DNA encod
Aac99336 DNA encod
Aac38651 Truncated
Aac70129 Antimicro
Aac94580 Cloned 3'
Aac87758 DNA encod

CC screening a Raphanus sativus seed cDNA library. This primer corresponds
 CC to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp
 CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a
 CC 123bp product, which was further reamplified with the same primers and
 CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
 CC product. This was used to screen a lambda ZAPII cDNA library by in situ
 CC plaque hybridisation. Positive plaques were purified and subjected to two
 CC additional screening rounds with the same probe. Inserts were excised in
 CC vivo into the pBluescript phagemid form with the aid of helper phage
 CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and
 CC their size compared by agarose gel electrophoresis. Four clones had
 CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
 CC of the 4 largest clones were then sequenced and found to differ only in
 CC the length of their 5' and 3' UTR's. The longest sequence is given here.
 CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Query Match 100.0%; Score 414; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 3.8e-92;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GTTTATTAGTCATCGGCTAAGTTTGGCTGCATCATCGCACTTCTTTTCTGCTCTT 60
DB |||||
DB 1 GTTTATTAGTCATCGGCTAAGTTTGGCTGCATCATCGCACTTCTTTTCTGCTCTT 60
QY 61 GTTCTTTTGTCTGTTTCGAAGCACCACCAATGTTGGAAGCAGAGAAGTTGTGCGAAAGG 120
DB |||||
DB 61 GTTCTTTTGTCTGTTTCGAAGCACCACCAATGTTGGAAGCAGAGAAGTTGTGCGAAAGG 120
QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAAACAATAAGCGCATGCAAGAAATCAGTGCATT 180
DB |||||
DB 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAAACAATAAGCGCATGCAAGAAATCAGTGCATT 180
QY 181 AACCTTGAGAAAGCAGACATGGAATCTTGCATCTATGTTCTTCCAGCTCACAAGTGTATC 240
DB |||||
DB 181 AACCTTGAGAAAGCAGACATGGAATCTTGCATCTATGTTCTTCCAGCTCACAAGTGTATC 240
QY 241 TGTACTTTCTCTTGTAAATTTATCGAAACTCTTTTGTGAATAGTTTATGTAATTTAC 300
DB |||||
DB 241 TGTACTTTCTCTTGTAAATTTATCGAAACTCTTTTGTGAATAGTTTATGTAATTTAC 300
QY 301 ACAAAATAAGTCAGTGCATCTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
DB |||||
DB 301 ACAAAATAAGTCAGTGCATCTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414
DB |||||
DB 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414

```

RESULT 2

AAQ70128 standard; cDNA; 414 BP.

```

XX AAQ70128;
XX AC
XX XX
XX 25-MAR-2003 (revised)
XX 14-FEB-1995 (first entry)
XX DE
XX DE Antimicrobial Rs-AFP1.
XX KW Antimicrobial; Rs-AFP1; symbiosis; disease-resistance; fungus-resistance;
XX KW Clavibacter xylis subsp. cynodontis; Cxc; crop improvement; endophyte; ss.
XX XX
XX OS Raphanus sativus.
XX XX
XX PN WO9416076-A1.
XX PD 21-JUL-1994.
XX PF
XX OS 05-JAN-1994; 94WO-GB000012.
XX XX

```

PR 08-JAN-1993; 93GB-00000281.

XX (ZENE) ZENECA LTD.

XX Dubock AC, Powell KA, Rees SB;

XX WPI; 1994-249223/30.

XX P-PSDB; AAR57325.

XX Antimicrobial protein producing endo-symbiotic microorganisms - is
 PT produced by combining nucleic acids encoding the protein with an
 PT endophyte, useful for protecting plant hosts from esp. fungal disease.

XX Disclosure; Page 31; 39pp; English.

XX Plant-derived antimicrobial proteins are expressed in endosymbiotic
 CC Clavibacter xylis subsp. cynodontis (Cxc). Plants or seeds treated with
 CC recombinant Cxc are protected against fungal disease. A suitable
 CC antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA
 CC sequence of Rs-AFP1 is given in AAQ70128. (Updated on 25-MAR-2003 to
 CC correct PN field.)

SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Query Match 100.0%; Score 414; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 3.8e-92;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTTTATTAGTCATCGGCTAAGTTTGGCTGCATCATCGCACTTCTTTTCTGCTCTT 60
DB |||||
DB 1 GTTTATTAGTCATCGGCTAAGTTTGGCTGCATCATCGCACTTCTTTTCTGCTCTT 60
QY 61 GTTCTTTTGTCTGTTTCGAAGCACCACCAATGTTGGAAGCAGAGAAGTTGTGCGAAAGG 120
DB |||||
DB 61 GTTCTTTTGTCTGTTTCGAAGCACCACCAATGTTGGAAGCAGAGAAGTTGTGCGAAAGG 120
QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAAACAATAAGCGCATGCAAGAAATCAGTGCATT 180
DB |||||
DB 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAAACAATAAGCGCATGCAAGAAATCAGTGCATT 180
QY 181 AACCTTGAGAAAGCAGACATGGAATCTTGCATCTATGTTCTTCCAGCTCACAAGTGTATC 240
DB |||||
DB 181 AACCTTGAGAAAGCAGACATGGAATCTTGCATCTATGTTCTTCCAGCTCACAAGTGTATC 240
QY 241 TGTACTTTCTCTTGTAAATTTATCGAAACTCTTTTGTGAATAGTTTATGTAATTTAC 300
DB |||||
DB 241 TGTACTTTCTCTTGTAAATTTATCGAAACTCTTTTGTGAATAGTTTATGTAATTTAC 300
QY 301 ACAAAATAAGTCAGTGCATCTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
DB |||||
DB 301 ACAAAATAAGTCAGTGCATCTATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360
QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414
DB |||||
DB 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414

```

RESULT 3

AAQ72333

ID AAT72333 standard; cDNA; 414 BP.

XX AAT72333;

XX 25-MAR-2003 (revised)

XX 19-JAN-1998 (first entry)

XX Raphanus sativus antifungal protein I (Rs-AFP1) cDNA.

XX Antifungal protein; candida; fungal resistance; food additive; radish;
 KW crop protection; plant defensin; bacterium; bacterial protection; preservative; ss.
 XX OS Raphanus sativus.

FH Key Location/Qualifiers
 FT 16..258
 FT /*tag= a
 FT sig_peptide 16..102
 FT /*tag= b
 FT mat_peptide 103..255
 FT /*tag= c
 FT /product= "antifungal_protein_1"
 XX WO9721815-A2.
 XX 19-JUN-1997.
 XX 12-DEC-1996; 96WO-GB003068.
 XX 13-DEC-1995; 95GB-00025455.
 XX 28-MAR-1996; 96GB-00006552.
 XX (ZENE) ZENECA LTD.
 XX Meleen RH, Puijk WC, Schaaper WMM, Sijtsma L, Van Amerongen A;
 PI Broekaert W, Samblanx GW, Fant F, Borremans FAM, Rees SB,
 PI Van Gelder WWJ;
 XX WPI; 1997-332785/30.
 XX P-PSDB; AAW19280.
 XX
 XX Antifungal peptide derived from radish antifungal protein 2 - and related
 PT DNA, useful for producing plants with increased fungal resistance and as
 PT therapeutic or preservative agent.
 XX
 XX Claim 8; Fig 2; 65pp; English.
 XX
 XX This cDNA sequence encodes an Rhanus sativus (radish) antifungal
 CC protein (Rs-APPI). Analogues of the homologous protein, Rs-APP2
 CC (AAW19281), have also been produced (see AAW19282-92, AAW19294-98,
 CC AAW19301-04, AAW19330-34 and AAW31765-834). Plants containing DNA
 CC sequences encoding these proteins have improved resistance to fungi.
 CC Compositions containing the peptides can be used to control fungi or
 CC bacteria in pharmaceutical (e.g. treatment of Candida infections) or
 CC preservative purposes (as food additives). In agriculture, the peptide
 CC may be used to improve disease resistance or disease tolerance of crops,
 CC either pre or post harvest. When applied to plants they may also have
 CC curative as well as protective actions. The peptides may also be used to
 CC protect plants by introducing them, or a microorganism capable of
 CC expressing the peptide into the soil. (Updated on 25-MAR-2003 to correct
 CC PI field.)
 XX
 XX SQ Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
 Query Match 100.0%; Score 414; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 3.8e-92;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTTATTAGTATGCTAGTAAAGTTGGTCCATCAGCACTCTTTTCTGCTCTT 60
 DB 1 GTTTATTAGTATGCTAGTAAAGTTGGTCCATCAGCACTCTTTTCTGCTCTT 60
 QY 61 GTTCTTTTGTCTTTTGAAGCACCACCAATGGTGGAGCAGCAAGTTGTGCGAAGG 120
 DB 61 GTTCTTTTGTCTTTTGAAGCACCACCAATGGTGGAGCAGCAAGTTGTGCGAAGG 120
 QY 121 CCAAGTGGGACATGTCAGAGTCTGTGGAACATACGATGCAAGTCAAGTCAAT 180
 DB 121 CCAAGTGGGACATGTCAGAGTCTGTGGAACATACGATGCAAGTCAAGTCAAT 180
 QY 181 AACCTTGAGAAACACGACATGATCTTGCACACTATGCTCCAGCTCACAAGTGTATC 240
 DB 181 AACCTTGAGAAACACGACATGATCTTGCACACTATGCTCCAGCTCACAAGTGTATC 240
 QY 241 TGTACTTCTCTTGTAAATTATCGCAAACTCTTTGGTGAATAGTTTTATGTAATTAC 300

Db 241 TGCTACTTCTCTTGTAAATTATCGCAAACTCTTTGGTGAATAGTTTTATGTAATTAC 300
 QY 301 ACAAAATAAGTCACTGCTCACTATCCATGAGTCAATTTTAAGACATGTACAGATATGTTAT 360
 Db 301 ACAAAATAAGTCACTGCTCACTATCCATGAGTCAATTTTAAGACATGTACAGATATGTTAT 360
 QY 361 GTTGGTTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414
 Db 361 GTTGGTTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414

RESULT 4

AAT68696
 ID AAT68696 standard; cDNA; 414 BP.

XX AAT68696;

DT 13-DEC-1997 (first entry)

XX Radish antifungal protein 1 (Rs-APPI) cDNA.

XX Rs-APPI; radish antifungal protein 1; fungicide; salt tolerance;
 KW preservative; transgenic plant; crop protection.
 XX

OS Raphanus sativus.

XX Key Location/Qualifiers

FT CDS 16..258

FT /*tag= a

FT /transl_except= (pos:85..87, aa:Glu)

FT sig_peptide 16..102

FT /*tag= b

FT mat_peptide 103..255

FT /*tag= c

XX WO9721814-A1.

XX 19-JUN-1997.

XX 12-DEC-1996; 96WO-GB003065.

XX 13-DEC-1995; 95GB-00025474.

XX (ZENE) ZENECA LTD.

XX Broekaert WF, De Samblanx GW, Rees SB;

XX WPI; 1997-332785/30.

XX P-PSDB; AAW19617.

XX New active mutants of radish antifungal protein 2 - used to generate
 PT fungus-resistant plants or as therapeutic or preservative agents.
 XX
 XX Disclosure; Fig 2; 39pp; English.

CC This cDNA clone codes for the preprotein for radish antifungal protein 1
 CC (Rs-APPI) (AAW19617). Novel antifungal proteins are based on Rs-APPI, Rs-
 CC APP2 (see AAW19616), Rs-APP3 and Rs-APP4, especially those in which Gly9
 CC is replaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by
 CC Met. Mutants (see AAW26371-90) of Rs-APP2 are specifically claimed. The
 CC mutants show improved salt tolerant antifungal activity, particularly
 CC when expressed in plants

XX Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

Query Match 100.0%; Score 414; DB 2; Length 414;

Best Local Similarity 100.0%; Pred. No. 3.8e-92;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATGCTAGTAAAGTTGGTCCATCAGCACTCTTTTCTGCTCTT 60

DB 1 GTTTATTAGTATGCTAGTAAAGTTGGTCCATCAGCACTCTTTTCTGCTCTT 60

QY 61 GTTCTTTTTCCTGCTTTTCGAGACACCAACATGAGTGGAGACACAGAGTGTGCGAAGG 120
 Db 61 GTTCTTTTTCCTGCTTTTCGAGACACCAACATGAGTGGAGACACAGAGTGTGCGAAGG 120
 QY 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGATGCAAGATCAGTGCATT 180
 Db 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGATGCAAGATCAGTGCATT 180
 QY 181 AACCTTGAGAAAGCAGCAGATGATCTTGAACATATGCTTCCAGCTCACAAGTGTATC 240
 Db 181 AACCTTGAGAAAGCAGCAGATGATCTTGAACATATGCTTCCAGCTCACAAGTGTATC 240
 QY 241 TGCTACTTTCCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
 Db 241 TGCTACTTTCCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
 QY 301 ACAAAATAGTCAGTGTCACTATCCATGAGTGAATTTTAAACATGTCACAGATGTTAT 360
 Db 301 ACAAAATAGTCAGTGTCACTATCCATGAGTGAATTTTAAACATGTCACAGATGTTAT 360
 QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414
 Db 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414

RESULT 5

ADCS1221
 ID ADCS1221 standard; DNA; 394 BP.
 XX AC ADCS1221;
 XX DT 18-DEC-2003 (first entry)
 XX DE Brassica oleracea defensin protein coding sequence.
 XX KW antimicrobial protein; defensin; transgenic plant;
 KW composite disease resistance; pathogenic bacteria;
 KW rice white leaf blight; brown-stripe disease; glume blight;
 KW seedling damping-off disease; filamentous fungi; rice blight;
 KW sheath blight disease; leaf blight; gene; ds.
 XX OS Brassica oleracea.
 XX FH Key Location/Qualifiers
 FT CDS 1..243
 FT /*tag= a
 FT /product= "Brassica oleracea defensin protein"
 XX PN JP2003088379-A.
 XX PD 25-MAR-2003.
 XX PF 18-SEP-2001; 2001JLP-00283117.
 XX PR 18-SEP-2001; 2001JLP-00283117.
 XX PA (DOKU-) DOKURITSU GYOSHI HOJIN NOGYO SEIBUTSU SH.

XX WPI; 2003-621123/59.
 XX P-PSDB; ADCS1222.
 XX PT Novel protein from Brassica campestris, useful as antimicrobial against
 PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for
 PT treating e.g. rice white leaf blight and sheath blight disease.
 XX PS Claim 3; SEQ ID NO 1; 34pp; Japanese.
 XX CC The invention comprises the amino acid and coding sequences of
 CC antimicrobial (defensin) proteins from Brassica. The DNA and protein
 CC sequences of the invention are useful for producing transformed plants
 CC with composite disease resistance, especially resistant to diseases
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-
 CC stripe disease, glume blight, and seedling damping-off disease. As well

CC as diseases caused by filamentous fungi, such as: rice blight, sheath
 CC blight disease, and leaf blight. The present DNA sequence encodes a
 CC Brassica defensin protein of the invention.

XX SQ Sequence 394 BP; 116 A; 71 C; 82 G; 125 T; 0 U; 0 Other;

Query Match 78.2%; Score 323.8; DB 9; Length 394;
 Best Local Similarity 90.4%; Pred. No. 5.6e-70;
 Matches 357; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY 16 ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTGCTCTTGTCTTTTGGCTGT 75
 Db 1 ATGGCTAAGTTTGGCTCCATCATCGCACTCTTTTGGCTGCTCTTGTCTTTTGGCTGT 60
 QY 76 TTCGAAGCACCACCAATGCTGGAGGACAGAGTGTGCAAGGCGCAAGTGGGACATGG 135
 Db 61 CTCGAAGCACCACCAATGCTGGAGGACAGAGTGTGCAAGGCGCAAGTGGGACATGG 120
 QY 136 TCAGGAGTCTGTGGAAACAATAACGATGCAAGATCAGTGCATTAACCTTGAGAAAGCA 195
 Db 121 TCAGGAGTCTGTGGAAACAATAACGATGCAAGATCAGTGCATTAACCTTGAGAAAGCA 180
 QY 196 CGACATGATCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGCTACTTTCCCTTGT 255
 Db 181 CGACATGATCTTGCACATATGCTTCCAGCTCACAAGTGTATCTGCTACTTTCCCTTGT 240
 QY 256 TAATTTATGCAAACTCTTTGGTGAATAGTTTATGTAATTTATGTAATTTATGTAAT 315
 Db 241 TAATTTATGCAAACTCTTTGGTGGTGTAGTTTGTGTAATTTATGTAATTTATGTAAT 300
 QY 316 GTCATATCCATGAGTGAATTTTAAAGATGTCACAGATGTCATGTTGTTGGTGGTTATA 375
 Db 301 GTCATATCAATGAGTGAATTTTATGATGATGTCATGATGATGATGATGATGATGAT 360
 QY 376 CAATAAAGTTTATTCACCAAAAAAATAAAAAA 410
 Db 361 -ATATAAAGTTTATTCACCAAAAAAATAAAAAA 394

RESULT 6

ADCS1223
 ID ADCS1223 standard; DNA; 426 BP.
 XX AC ADCS1223;
 XX DT 18-DEC-2003 (first entry)
 XX DE Brassica defensin protein coding sequence.
 XX KW antimicrobial protein; defensin; transgenic plant;
 KW composite disease resistance; pathogenic bacteria;
 KW rice white leaf blight; brown-stripe disease; glume blight;
 KW seedling damping-off disease; filamentous fungi; rice blight;
 KW sheath blight disease; leaf blight; gene; ds.
 XX OS Brassica sp.
 XX FH Key Location/Qualifiers
 FT CDS 1..243
 FT /*tag= a
 FT /product= "Brassica defensin protein"
 XX PN JP2003088379-A.
 XX PD 25-MAR-2003.
 XX PF 18-SEP-2001; 2001JLP-00283117.
 XX PR 18-SEP-2001; 2001JLP-00283117.
 XX PA (DOKU-) DOKURITSU GYOSHI HOJIN NOGYO SEIBUTSU SH.
 XX WPI; 2003-621123/59.

DR P-PSDB; ADC51224.
 XX Novel protein from Brassica campestris, useful as antimicrobial against
 PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for
 PT treating e.g. rice white leaf blight and sheath blight disease.
 XX Claim 3; SEQ ID NO 3; 34pp; Japanese.
 PS
 CC The invention comprises the amino acid and coding sequences of
 CC antimicrobial (defensin) proteins from Brassica. The DNA and protein
 CC sequences of the invention are useful for producing transformed plants
 CC with composite disease resistance, especially resistant to diseases
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-
 CC stripe disease, glume blight, and seedling damping-off disease. As well
 CC as diseases caused by filamentous fungi, such as: rice blight, sheath
 CC blight disease, and leaf blight. The present DNA sequence encodes a
 CC Brassica defensin protein of the invention.
 XX
 SQ Sequence: 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;
 Query Match 74.3%; Score 307.8; DB 9; Length 426;
 Best Local Similarity 88.8%; Pred. No. 4.9e-66;
 Matches 356; Conservative 0; Mismatches 42; Indels 3; Gaps 2;
 QY 16 ATGCTAAGTTTGGTCCATCATCGACCTCTTTTGGCTGCTCTTTTGGTCTCTTTTGGTCT 75
 Db 1 ATGCCCAAGTTTGTCTATCATTTGCCCACTTTTGGCTGCTCTTTTGGTCTCTTTTGGTCT 60
 QY 76 TTCGAAGCACCACCAATGGTGGAGCAGACAGAGTTGTGGAGAGGCCAGTGGACATGG 135
 Db 61 TTCGAGCACCACCAATGGTGGAGCAGAGTTGTGGAGAGGCCAGTGGACATGG 120
 QY 136 TCAGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATTAACCTTGAGAAAGCA 195
 Db 121 TCAGAGTCTGTGGAAACAATAACGCATGCAAGATCAGTGCATTAACCTTGAGAAAGCA 180
 QY 196 CGACATGATCTTGCACATATCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTTGT 255
 Db 181 CGACATGATCTTGCACATATCTTCCAGCTCACAAGTGTATCTGCTACTTCTCTTGT 240
 QY 256 TAATTTATCGCAAACTCTTTGGTGAATAGTTTTATGTAATTTACACAAAATAAGTCAGT 315
 Db 241 TAATTTATCGCAAACTCTTTGGTGGTGTAGTTTGTGTAATTTACATAAATAAGTCTGT 300
 QY 316 GTCACTATCCATGAGTGATTTTAAGACATGTACC--AGATATCTTATGTGTGTTTCGGTTA 373
 Db 301 GTCACTATCAATGAGTGATTTTATGACATGTACCTGATATATGTTATGTGTTTCGGTTA 360
 QY 374 TACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414
 Db 361 TA-ATAAAGTTTATGCAACCTTCAAAAAAATAAAAAA 400

RESULT 7
 AAA53190
 ID AAA53190 standard; DNA; 449 BP.
 XX
 AC AAA53190;
 XX
 XX 06-OCT-2000 (first entry)
 DT
 DE Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.
 XX
 KW Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;
 KW pathogenic microbe; radish; rice blast disease; ds.
 XX
 OS Raphanus sativus.
 XX JP2000116379-A.
 FN
 XX 25-APR-2000.
 PD
 XX 09-OCT-1998; 98JP-00288472.
 PF

XX 09-OCT-1998; 98JP-00288472.
 PR (TOYA-) TOYAMA KEN.
 PA
 XX WPI; 2000-389821/34.
 DR P-PSDB; AAY91117.
 XX
 PT Isolated DNA from Raphanus sativus used to transform a microbe and a
 PT plant to produce an antibacterial protein used to increase resistance of
 PT rice paddy against pathogenic microbes.
 PS
 CC Claim 1; Page 4; 7pp; Japanese.
 XX
 CC The present sequence encodes an antibacterial protein, designated
 CC radishin, isolated from Raphanus sativus (radish). A phage or plasmid
 CC comprising radishin can be used for increasing resistance of paddy and
 CC rice blast disease against pathogenic microbes
 XX
 SQ Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;
 Query Match 61.6%; Score 255; DB 3; Length 449;
 Best Local Similarity 81.0%; Pred. No. 4.7e-53;
 Matches 333; Conservative 0; Mismatches 74; Indels 4; Gaps 3;
 QY 4 TTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCATTCTTTTGGTCTCTTTGTT 63
 Db 29 TTATTAGTATCATGGCTAAGTTTGGTCCATCATCGCATTCTTTTGGTCTCTTTGTT 88
 QY 64 CTTTTTGGTCTCTTTTGGAGCACCACCAATGGTGGAGCAGCAAGTTTGGCAAGGCCA 123
 Db 89 GTTTTTCTCTTTTGGAGCACCACCAATGGTGGAGCAGCAAGTTTGGTCCAGAGCCA 148
 QY 124 AGTGGAGCATGGTCCAGAGTCTCTGGAACAATAACGATGCAAGATCAGTGCATTAC 183
 Db 149 AGTGGAGCATGGTCCAGAGTCTCTGGAACAATAACGATGCAAGATCAGTGCATTAC 208
 QY 184 CTTGAGAAAGCAGCATGATGCTTCCAACTATGCTTCCAGCTCACAAGTGTATCTGTC 243
 Db 209 CTTGAGAAAGCAGCATGATGCTTCCAACTATGCTTCCAGCTCACAAGTGTATCTGTC 268
 QY 244 TACTTCTCTTGTATTT-TATCGCAAACTCTTTGGTGAATAGTTT--TTATGTAATTTAC 300
 Db 269 TATTCCCTTGTATTTCCATAAACTCTTCCGTTGGTTAATAGTGTGCGCATTTACATAT 328
 QY 301 ACAAAATAAGTCACTGCTCACTATCCATGATGATTTTAAGACATCTACACAGATATG-TTA 359
 Db 329 AATTAATAGTTTGTCTCACTATTTTATGACATCTTTATGACATGTGCGAGTATGTTTA 388
 QY 360 TGTGTTCCGTTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 410
 Db 389 TGTGTTCCGTTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 439

RESULT 8
 AAQ38652
 ID AAQ38652 standard; DNA; 261 BP.
 XX
 AC AAQ38652;
 XX
 XX 25-MAR-2003 (revised)
 DT 07-JUL-1993 (first entry)
 DT
 DE Rs-APF2 cDNA.
 XX
 KW Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
 KW fungicide; bacteriocide; antibiotic; antifungal; gram positive;
 KW plant disease resistance; low toxicity.
 XX
 OS Raphanus sativus.
 XX
 XX Key Location/Qualifiers
 FH 16..256
 FT CDS

/*tag= a

FT XX WO9305153-Al.
 PN XX 18-MAR-1993.
 PD XX 27-AUG-1992; 92WO-GB001570.
 PF XX 29-AUG-1991; 91GB-00018523.
 PR XX 13-FEB-1992; 92GB-00003038.
 PR XX 25-JUN-1992; 92GB-00013526.
 XX (ICIL) IMPERIAL CHEM IND PLC.
 PA Broekxaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;
 PI Vanderleyden J;
 PN WPI; 1993-100978/12.
 DR XX
 XX
 XX Biocidal proteins isolated from seeds of plants - e.g. brassica or
 PT dahlia, useful for increasing plants' resistance to fungal and bacterial
 PT diseases.
 XX
 PS Example 21; Fig 35; 110pp; English.
 XX
 CC This cDNA represents the sequence of Rs-APP2 from *Raphanus sativus*. PCR
 CC primer AAQ38640 was used together with AAQ38641 to generate a probe for
 CC screening a *Raphanus sativus* seed cDNA library. This primer corresponds
 CC to amino acids 2 to 7 of Rs-APP1 and has a sense orientation. The 144bp
 CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a
 CC 123bp product, which was further reamplified with the same primers and
 CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR
 CC product. This was used to screen a lambda ZAPII cDNA library by in situ
 CC plaque hybridisation. Positive plaques were purified and subjected to two
 CC additional screening rounds with the same probe. Inserts were excised in
 CC vivo into the pBluescript phagemid form with the aid of helper phage
 CC R408. Inserts from 22 positive clones were excised by EcoRI digestion and
 CC their size compared by agarose gel electrophoresis. Four clones had
 CC insert sizes of approx. 400bp the others between 250-300bp. The inserts
 CC of the 4 largest clones were then sequenced and found to differ only in
 CC the length of their 5' and 3' UTR's. The longest sequence was identified
 CC as Rs-APP1 (AAQ38650). Rs-APP2 was seen to differ by only 2 amino acids
 CC from Rs-APP1, so the Rs-APP1 cDNA was transformed to the Rs-APP2
 CC nucleotide sequence by PCR assisted site directed mutagenesis. (Updated
 CC on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;

Query Match 61.4%; Score 254.2; DB 2; Length 261;
 Best Local Similarity 98.8%; Pred. No. 6.5e-53;
 Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTGATCATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGGCTGCTTT 60
 DB 1 GTTTTATTAGTGATCATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGGCTGCTTT 60
 QY 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATGGTGGAGCAGCAAGTTGTGCGAAGG 120
 DB 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATGGTGGAGCAGCAAGTTGTGCGAAGG 120
 QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAAGCGATGCAAGTAATCAGTGCATT 180
 DB 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAAGCGATGCAAGTAATCAGTGCATT 180
 QY 181 AACCTTGAGAAAGCAGCATGGATCTTTGCAACTATGTCTTCCAGCTCACAAAGTGATC 240
 DB 181 AGACTTGAAGAAAGCAGCATGGATCTTTGCAACTATGTCTTCCAGCTCACAAAGTGATC 240
 QY 241 TGCTACTTTCTCTGTTAAT 259
 DB 241 TGCTACTTTCTCTGTTAAT 259

RESULT 9
 AAQ70130
 ID AAQ70130 standard; cDNA; 288 BP.
 XX
 AC AAQ70130;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-FEB-1995 (first entry)
 DE Antimicrobial Rs-APP2.
 XX
 KW Antimicrobial; Rs-APP2; symbiosis; disease-resistance; fungus-resistance;
 KW Clavibacter xyl. subsp. cynodontis; Cxc; crop improvement; endophyte;
 KW PCR; polymerase chain reaction; mutagenesis; ss.
 XX
 OS *Raphanus sativus*.
 PN WO9416076-Al.
 XX
 PD 21-JUL-1994.
 XX
 PF 05-JAN-1994; 94WO-GB000012.
 XX
 PR 08-JAN-1993; 93GB-00000281.
 XX
 PA (ZENE) ZENECA LTD.
 XX
 PI Dubock AC, Powell KA, Rees SB;
 XX
 DR WPI; 1994-249223/30.
 DR P-PSDB; AAR57327.
 XX
 PT Antimicrobial protein producing endo-symbiotic microorganisms - is
 PT produced by combining nucleic acids encoding the protein with an
 PT endophyte, useful for protecting plant hosts from esp. fungal disease.
 XX
 PS Disclosure; Page 33; 39pp; English.
 XX
 CC Plant-derived antimicrobial proteins are expressed in endosymbiotic
 CC Clavibacter xyl. subsp. cynodontis (Cxc). Plants or seeds treated with
 CC recombinant Cxc are protected against fungal disease. A suitable
 CC antimicrobial protein is Rs-APP1 from *R. sativus*. The full-length cDNA
 CC sequence of PCR assisted site-directed mutagenesis of Rs-APP2 is given in
 CC AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX
 SQ Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;

Query Match 61.4%; Score 254.2; DB 2; Length 288;
 Best Local Similarity 98.8%; Pred. No. 6.6e-53;
 Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTGATCATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGGCTGCTTT 60
 DB 28 GTTTTATTAGTGATCATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGGCTGCTTT 87
 QY 61 GTTCTTTTGTGCTTTTGAAGCACCACCAATGGTGGAGCAGCAAGTTGTGCGAAGG 120
 DB 88 GTTCTTTTGTGCTTTTGAAGCACCACCAATGGTGGAGCAGCAAGTTGTGCGAAGG 147
 QY 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAAGCGATGCAAGTAATCAGTGCATT 180
 DB 148 CCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAAGCGATGCAAGTAATCAGTGCATT 207
 QY 181 AACCTTGAGAAAGCAGCATGGATCTTTGCAACTATGTCTTCCAGCTCACAAAGTGATC 240
 DB 208 AGACTTGAAGAAAGCAGCATGGATCTTTGCAACTATGTCTTCCAGCTCACAAAGTGATC 267
 QY 241 TGCTACTTTCTCTGTTAAT 259
 DB 268 TGCTACTTTCTCTGTTAAT 286

```

RESULT 10
AAV10632
ID AAV10632 standard; DNA; 403 BP.
XX
AC AAV10632;
XX
DT 23-JUN-1998 (first entry)
XX
DE A. thaliana PDF1.1 DNA.
XX
KW Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;
KW fungi; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 26..288
FT sig_peptide /*tag= a
FT mat_peptide /*tag= b
FT /*tag= c
FT /product= "PDF1.1"
FT /note= "plant defensin"
XX
FN WO9800023-A2.
XX
PD 08-JAN-1998.
XX
PF 20-JUN-1997; 97MO-GB001672.
XX
PR 01-JUL-1996; 96GB-00013753.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras FRG, Manners JM;
PI Kazan K;
XX
DR WPI; 1998-086663/08.
DR P-PSDB; AAW40345.
XX
PT Protecting plants against pathogens by inducing defensin genes - by
PT stimulating ethylene or jasmonate pathways, also new promoter of defense
PT gene from Arabidopsis.
XX
PS Disclosure; Fig 1; 72pp; English.
XX
CC This sequence encodes the Arabidopsis PDF1.1 gene which is used in a
CC novel method for the protection of plants against pathogens which
CC involves inducing expression of a plant defensin gene by stimulating the
CC jasmonate and/or ethylene pathways. The method is used to induce
CC protection against necrotrophic pathogens, specifically fungi and does
CC not require cytotoxic or potentially harmful chemicals
XX
SQ Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;
Query Match 58.6%; Score 242.4; DB 2; Length 403;
Best Local Similarity 76.5%; Pred. No. 5.7e-50;
Matches 297; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY 1 GTTTTATAGTATGATGGCTAAGTTTGGTCCATCGCATCTTTTCTGCTCTT 60
DB 11 GTTAAACATAGTCATGGCTAAGTCTGCTACATCGTCTTCTTCGCTGCTCT 70
QY 61 GTTCTTTTGTCTTTCGAGCACCACCAATGGTGGAGACACAGAGTTTGCGAAGG 120
DB 71 GTTTTCTTTGTCTTCTGAAGCACCAGATGGTGGAGACACAGAGTTTGCGAGAG 130
QY 121 CCAAGTGGACATGGTCAGAGTCTGTGGAACAAATACCGATGCAAGATCGTCAAT 180
DB 131 CCAAGTGGACATGGTCGGAGTTTGGGAAACAGTAACCGGTGCAAGATCGTCAAT 190
QY 181 AACCTTGAGAAAGACACATGGATCTTGCAACTATGCTTCCAGTCACCAAGTGTATC 240

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DB 191 AACCTTGAGAAAGACACATGGATCTTGCAACTATGCTTCCAGCTCACAAATGATC 250
QY 241 TGTACTTCTCTGTTTAAATTTATCGCAAACTCTTGGTGAATAGTTTATGTAATTTAC 300
DB 251 TGTACTTCCCATGTTAATCTACCAAGAGCTCTTAATGCTTAATTATAAGTGTGATTT 310
QY 301 ACAAATAAGTCAGTGCATCTATCCATGATGAGTGAATTTAAGACATGTACCAGATGTTAT 360
DB 311 CTATTAAATAAGTATGTGCTCACTCTATGAGAGCTCTTATGACATGTACCAGATGTTAT 370
QY 361 GTTGGTTCGGTTATACAAATAAAGTTTT 388
DB 371 GTTGTCTTGTGTTTAAAGGTAACCTTT 398

RESULT 11
AAZ99339
ID AAZ99339 standard; DNA; 575 BP.
XX
AC AAZ99339;
XX
DT 03-JUL-2000 (first entry)
XX
DE DNA encoding a fusion protein of DmAMP1 and RsAPP2.
XX
KW Antimicrobial protein; AMP1; transgenic plant; linker peptide;
KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.
XX
OS Synthetic.
OS Dahlia merckii.
XX Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 3..566
FT /*tag= a
FT /product= "fusion protein of DmAMP1 and RsAPP2"
XX
PN WO200011175-A1.
XX
PD 02-MAR-2000.
XX
PF 17-AUG-1999; 99WO-GB002716.
XX
PR 18-AUG-1998; 98GB-00018001.
PR 04-DEC-1998; 98GB-00026753.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
PI WPI; 2000-246564/21.
DR P-PSDB; AAY84072.
XX
PT Improving expression of polyproteins in plants involves coexpression of
PT two or more proteins in plants within a single transcription unit.
XX
PS Disclosure; Fig 34; 151pp; English.
XX
CC The present sequence encodes a protein of the invention, comprising the
CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
CC (AMP) 1 and the antifungal protein 2 (RsAPP2), linked by a linker
CC propeptide of the invention. The specification describes methods for
CC improving expression levels of one or more proteins in a transgenic
CC plant. The method comprises inserting a DNA sequence having a promoter
CC region operably linked to two or more protein encoding regions separated
CC by a DNA sequence coding for a linker propeptide and a terminator region.
CC The method is used to produce proteins in plants. The linker propeptide
CC comprising a cleavage site, whereby the expressed polyprotein is post-
CC translationally processed into the component protein molecules. The
CC propeptide sequence is rich in amino acids A, V, S and T and contains
CC dipeptidic sequences consisting of either two acidic, two basic or one
CC acidic and one basic residue as a cleavable linker sequence

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XX SQ Sequence 575 BP; 133 A; 137 C; 149 G; 156 T; 0 U; 0 Other;
Query Match 56.1%; Score 232.4; DB 3; Length 575;
Best Local Similarity 95.6%; Pred. No. 1.8e-47;
Matches 239; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 10 GTGATCATGCTAAGTTGGTCCATCATCGCAGCTTCTTTTGGCTGCTGCTGCTTTT 69
DB 318 GGGCCCATGCTAAGTTGGTCCATCATCGCAGCTTCTTTTGGCTGCTGCTGCTTTT 377
QY 70 GCTGCTTTTGAAGCACCACCAATGGTGAAGCAGACAGAGTTGTGGGAAGGCCAAAGTGGG 129
DB 378 GCTGCTTTTGAAGCACCACCAATGGTGAAGCAGACAGAGTTGTGGGAAGGCCAAAGTGGT 437
QY 130 ACATGTCAGAGTCTGTGAAACATTAAGCATGCAAGTCAAGTCAAGTCAAGTCAAGT 189
DB 438 ACATGTCAGAGTCTGTGAAACATTAAGCATGCAAGTCAAGTCAAGTCAAGTCAAGT 497
QY 190 AAAGCAGCATGATCTTGCACACTATGTTTCCAGCTCACAAGTGTATCTGCTACTTTT 249
DB 498 AAAGCAGCATGATCTTGCACACTATGTTTCCAGCTCACAAGTGTATCTGCTACTTTT 557
QY 250 CTTTGTAAAT 259
DB 558 CTTTGTAAAT 567
RESULT 12
AAV10633
ID AAV10633 standard; DNA; 400 BP.
AC AAV10633;
DT 23-JUN-1998 (first entry)
DE A. thaliana PDF1.2 DNA.
KW Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;
KW fungi; ss.
OS Arabidopsis thaliana.
XX Key Location/Qualifiers
FH 32..274
FT CDS /*tag= a
FT sig_peptide 32..119 /*tag= b
FT mat_peptide 120..271 /*tag= c
FT /*product= "PDF1.2"
FT /*note= "plant defensin"
XX WO9800023-A2.
XX 08-JAN-1998.
XX 20-JUN-1997; 97WO-GB001672.
XX 01-JUL-1996; 96GB-00013753.
XX (ZENE) ZENECA LTD.
XX Broekaert WF, Thomma BPHJ, Penninckx IAMA, Terras FRG, Manners JM;
PI Kazan K;
XX WPI; 1998-086663/08.
XX P-PSDB; AAW40346.
XX Protecting plants against pathogens by inducing defensin genes - by
PT stimulating ethylene or jasmonate pathways, also new promoter of defensin
PT gene from Arabidopsis.
XX

PS Disclosure; Fig 1; 72pp; English.
XX This sequence encodes the Arabidopsis PDF1.2 gene which is used in a
CC novel method for the protection of plants against pathogens which
CC involves inducing expression of a plant defensin gene by stimulating the
CC jasmonate and/or ethylene pathways. The method is used to induce
CC protection against necrotrophic pathogens, specifically fungi and does
CC not require cytotoxic or potentially harmful chemicals
XX
SQ Sequence 400 BP; 109 A; 82 C; 80 G; 125 T; 0 U; 4 Other;
Query Match 53.9%; Score 223; DB 2; Length 400;
Best Local Similarity 79.9%; Pred. No. 3.3e-45;
Matches 274; Conservative 0; Mismatches 67; Indels 2; Gaps 1;
QY 5 TATTAGTATCATGCTAAGTTTGGTCCATCATCGCAGCTTCTTTTGGCTGCTGCTGCTTC 64
DB 21 TATATATCATCATGCTAAGTTTGGTCCATCATCGCAGCTTCTTTTGGCTGCTGCTGCTTC 80
QY 65 TTTTGTCTGCTTTTGAAGCACCACCAATGGTGAAGCAGACAGAGTTGTGGAAAGGCCAA 124
DB 81 TCTTTGCTGCTTTTGAAGCACCACCAATGGTGAAGCAGACAGAGTTGTGGAAAGGCCAA 140
QY 125 GTGGGACATGTCAGAGTCTGTGAAACATTAAGCATGCAAGTCAAGTCAAGTCAAGTCAAC 184
DB 141 GTGGGACATGTCAGAGTCTGTGAAACATTAAGCATGCAAGTCAAGTCAAGTCAAGTCAAC 200
QY 185 TTTGAGAAAGCAGACATGGATCTTGCACACTATGTTTCCAGCTCACAAGTGTATCTGCT 244
DB 201 TTGAAGGAGCCAAACATGATCATGCAACTATGTTTCCAGCAGACACAAAGTGTATCTGTT 260
QY 245 ACTTCCCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTTTATGTAATTTACACAA 304
DB 261 AGTCCCATGTTAAATCTACCACTAATCTTTGGTCTAAATCGTGTGTTTATTTACATAAA 320
QY 305 AATAAGTCAGTGTCACTATCCATGATGATTTTAAGCATGTA 347
DB 321 AATAAGTCAGTGTCACTATCCATGATGATTTTAAGCATGTA 361
RESULT 13
AAT94581
ID AAT94581 standard; DNA; 500 BP.
AC AAT94581;
DT 12-MAY-1998 (first entry)
DE Composite cDNA sequence for Alyssum species antifungal polypeptide.
XX Antifungal polypeptide; AlyAFP; inhibition; transgenic plant;
KW phytopathogenic fungus; resistance; ss.
XX Alyssum sp.
XX WO9737024-A2.
XX 09-OCT-1997.
XX 27-MAR-1997; 97WO-US005709.
XX 29-MAR-1996; 96US-00627706.
XX (MONS) MONSANTO CO.
XX Liang J, Shah D, Wu Y, Rosenberger CA;
XX WPI; 1997-503109/46.
XX Alyssum antifungal polypeptide and corresponding DNA - used in the
PT production of transgenic plants resistant to phytopathogenic fungi.
XX Example 4; Page 67; 92pp; English.
PS


```
XX WPI: 2000-057353/05.
DR P-PSDB; ANY57565.
XX
PT An antibacterial protein gene of Wasabia japonica - useful as a food- or
PT feed-additive.
XX
PS Claim 3; Page 13-14; 16pp; Japanese.
XX
CC The present sequence encodes an antibacterial protein isolated from
CC Wasabia japonica. The antibacterial protein can be used as a food or feed
CC additive. (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 416 BP; 111 A; 77 C; 81 G; 147 T; 0 U; 0 Other;
Query Match 48.6%; Score 201; DB 3; Length 416;
Best Local Similarity 88.0%; Pred. No. 8.6e-40;
Matches 219; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
Qy 16 ATGGCTAAGTTGGCTCCATCGACATGCTTTTGGCTGCTCTTTGTTCTTTTGGTCT 75
Db 1 ATGGCTAAGTTGGCTTCTATCATCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
Qy 76 TTCGAAGCACCACCAATGGTGAAGCACAGAGTTGTGCAAGGCCAAAGTGGGACATGG 135
Db 61 TTGGAAGCACCACCAATGGTGAAGCCGACAGATTGTGCGAGAGTCAAGTGGGACATGG 120
Qy 136 TCAGGAGTCTGTGGAACAACAATACCGCATGCAAGATCAGTGCATTAACTTGAGAAAGCA 195
Db 121 TCAGGAGTCTGTGGAACAACAATACCGCATGCAAGATCAGTGCATTAACTTGAGGAGCA 180
Qy 196 CGACATGGATCTTGCAACTATGTTCTTCCAGCTCACAAGTGTATCTGTCTTCTTGT 255
Db 181 CGACATGGATCTTGCAACTATGTTCTTCCATATCCATATCAGATGATCTGTCTTCTTGT 240
Qy 256 TAATTATC 264
Db 241 TAATTATC 249
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Job time : 355 secs

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OM nucleic - nucleic search, using sw model

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Title: US-10-006-252A-19

Perfect score: 414

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Maximum Match 100%

Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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7	254.2	61.4	288	1	US-08-377-192-58
8	254.2	61.4	288	3	US-08-971-982-58
9	219	52.9	285	1	US-08-627-706-16
10	219	52.9	285	3	US-09-103-489-16
11	219	52.9	285	4	US-09-829-381D-16
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14	215.8	52.1	285	4	US-09-829-381D-17
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16	203.4	49.1	500	3	US-09-103-489-9
17	203.4	49.1	500	4	US-09-829-381D-9
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20	194.6	47.0	308	4	US-09-829-381D-5
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22	180	43.5	270	3	US-09-103-489-14
23	180	43.5	270	4	US-09-829-381D-14
24	178.8	43.2	286	1	US-08-627-706-12
25	178.8	43.2	286	3	US-09-103-489-12
26	178.8	43.2	286	4	US-09-829-381D-12
27	129.8	31.4	284	1	US-08-377-687-50

28 129.8 31.4 284 1 US-08-377-192-50
29 129.8 31.4 284 3 US-08-971-982-50
30 104.2 25.2 306 1 US-08-627-706-8
31 104.2 25.2 306 3 US-09-103-489-8
32 104.2 25.2 306 4 US-09-829-381D-8
33 74.6 18.0 243 4 US-09-732-210-11
34 50.8 12.3 150 1 US-08-377-687-33
35 50.8 12.3 150 1 US-08-377-687-34
36 50.8 12.3 150 1 US-08-777-192-33
37 50.8 12.3 150 1 US-08-777-192-34
38 50.8 12.3 150 3 US-08-971-982-33
39 50.8 12.3 150 3 US-08-971-982-34
40 50.6 12.2 565 4 US-09-589-733C-6
41 47.6 11.5 150 1 US-08-377-687-31
42 47.6 11.5 150 1 US-08-777-192-31
43 47.6 11.5 150 3 US-08-971-982-31
44 39.6 9.6 1318 4 US-09-719-108-5
45 39.2 9.5 568 1 US-08-582-257-20

ALIGNMENTS

RESULT 1
US-08-377-687-48
; Sequence 48, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
US-08-377-687-48

Sequence 50, Appl
Sequence 50, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 11, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 5, Appl
Sequence 20, Appl

Query Match 100.0%; Score 414; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 7.4e-107;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTTATTAGTATGATCGCTAAGTTTGGTCCATCATCGCACTCTTTTGGCTGCTCTT 60
DB 1 GTTTTATTAGTATGATCGCTAAGTTTGGTCCATCATCGCACTCTTTTGGCTGCTCTT 60
QY 61 GTTCTTTTGGCTGCTTTCGAAGCACCACCAATGTTGGAAGCAGCAAGTTCGCGAAAGG 120
DB 61 GTTCTTTTGGCTGCTTTCGAAGCACCACCAATGTTGGAAGCAGCAAGTTCGCGAAAGG 120
QY 121 CCAAGTGGACATGTCAGAGTCTGTCGAAACAATAACGATGCAAGATCAGTGCATT 180
DB 121 CCAAGTGGACATGTCAGAGTCTGTCGAAACAATAACGATGCAAGATCAGTGCATT 180
QY 181 AACCTTGAGAAAGCAGCATGATGTCGAAACAATAACGATGCAAGATCAGTGCATT 240
DB 181 AACCTTGAGAAAGCAGCATGATGTCGAAACAATAACGATGCAAGATCAGTGCATT 240
QY 241 TGCTACTTCTTCTGTTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTAC 300
DB 241 TGCTACTTCTTCTGTTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTAC 300
QY 301 ACAAATAAGTCACTATCCATGAGTGAATTTAAGACATGTCACAGATATGTTAT 360
DB 301 ACAAATAAGTCACTATCCATGAGTGAATTTAAGACATGTCACAGATATGTTAT 360
QY 361 GTTGGTTCGGTTATACAAATAAGTTTATTCACCAAAAAAAAAAAAAA 414
DB 361 GTTGGTTCGGTTATACAAATAAGTTTATTCACCAAAAAAAAAAAAAA 414

RESULT 2

US-08-777-192-48
; Sequence 48, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,192
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
; US-08-777-192-48
Query Match 100.0%; Score 414; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 7.4e-107;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTTATTAGTATGATCGCTAAGTTTGGTCCATCATCGCACTCTTTTGGCTGCTCTT 60
DB 1 GTTTTATTAGTATGATCGCTAAGTTTGGTCCATCATCGCACTCTTTTGGCTGCTCTT 60
QY 61 GTTCTTTTGGCTGCTTTCGAAGCACCACCAATGTTGGAAGCAGCAAGTTCGCGAAAGG 120
DB 61 GTTCTTTTGGCTGCTTTCGAAGCACCACCAATGTTGGAAGCAGCAAGTTCGCGAAAGG 120
QY 121 CCAAGTGGACATGTCAGAGTCTGTCGAAACAATAACGATGCAAGATCAGTGCATT 180
DB 121 CCAAGTGGACATGTCAGAGTCTGTCGAAACAATAACGATGCAAGATCAGTGCATT 180
QY 181 AACCTTGAGAAAGCAGCATGATGTCGAAACAATAACGATGCAAGATCAGTGCATT 240
DB 181 AACCTTGAGAAAGCAGCATGATGTCGAAACAATAACGATGCAAGATCAGTGCATT 240
QY 241 TGCTACTTCTTCTGTTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTAC 300
DB 241 TGCTACTTCTTCTGTTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTAC 300
QY 301 ACAAATAAGTCACTATCCATGAGTGAATTTAAGACATGTCACAGATATGTTAT 360
DB 301 ACAAATAAGTCACTATCCATGAGTGAATTTAAGACATGTCACAGATATGTTAT 360
QY 361 GTTGGTTCGGTTATACAAATAAGTTTATTCACCAAAAAAAAAAAAAA 414
DB 361 GTTGGTTCGGTTATACAAATAAGTTTATTCACCAAAAAAAAAAAAAA 414

RESULT 3

US-08-971-982-48
; Sequence 48, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,982
; FILING DATE: 17-No. 6187904-1997

CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/002,480
 FILING DATE: 04-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, PAUL N.
 REGISTRATION NUMBER: 16,773
 REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-861-3000
 TELEFAX: 202-822-0944
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 414 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 16..255
 SEQUENCE DESCRIPTION: SEQ ID NO: 48:
 US-08-971-982-48

Query Match 100.0%; Score 414; DB 3; Length 414;
 Best Local Similarity 100.0%; Pred. No. 7.4e-107;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTATGATGCTAAGTTTGGTCCCATCATCGCACTCTCTTTTCTGCTCTT 60
 DB 1 GTTTTATTAGTATGATGCTAAGTTTGGTCCCATCATCGCACTCTCTTTTCTGCTCTT 60

QY 61 GTTCTTTTCTGCTTTTCGAAGCACCACCAATGGTGGAAAGCAGAGTTGCGAAAGG 120
 DB 61 GTTCTTTTCTGCTTTTCGAAGCACCACCAATGGTGGAAAGCAGAGTTGCGAAAGG 120

QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAAGCATGCAAGTATGATGCAATT 180
 DB 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAAGCATGCAAGTATGATGCAATT 180

QY 181 AACCTTGAGAAAGCAGACATGATCTTGCACATATGTTCTCCAGCTCACAAGTGTATC 240
 DB 181 AACCTTGAGAAAGCAGACATGATCTTGCACATATGTTCTCCAGCTCACAAGTGTATC 240

QY 241 TGTACTTTCTGTTAAATTTATCGAAACTCTTTGGTGAATAGTTTTATGTAATTTAC 300
 DB 241 TGTACTTTCTGTTAAATTTATCGAAACTCTTTGGTGAATAGTTTTATGTAATTTAC 300

QY 301 ACAAATAAGTCACTGCTCACTATCCATGATGATTTTAAAGCATGTACAGATATGTTAT 360
 DB 301 ACAAATAAGTCACTGCTCACTATCCATGATGATTTTAAAGCATGTACAGATATGTTAT 360

QY 361 GTTGGTTCGTTATACAAATAAAGTTTATTACCAAAAAA 414
 DB 361 GTTGGTTCGTTATACAAATAAAGTTTATTACCAAAAAA 414

RESULT 4
 US-09-077-951-19
 Sequence 19, Application US/09077951
 Patent No. 6372888
 GENERAL INFORMATION:
 APPLICANT: De Samblanx, Geneveva
 APPLICANT: Broekaert, Willem
 APPLICANT: Rees, Sarah
 TITLE OF INVENTION: Antifungal Proteins
 FILE REFERENCE: PPD50093
 CURRENT APPLICATION NUMBER: US/09/077,951
 CURRENT FILING DATE: 1999-03-11
 EARLIER APPLICATION NUMBER: GB 9525474.4
 EARLIER FILING DATE: 1995-12-13
 EARLIER APPLICATION NUMBER: PCT/GB96/03065
 EARLIER FILING DATE: 1996-12-12

NUMBER OF SEQ ID NOS: 77
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 19
 LENGTH: 414
 TYPE: DNA
 ORGANISM: Raphanus sativus
 US-09-077-951-19

Query Match 100.0%; Score 414; DB 4; Length 414;
 Best Local Similarity 100.0%; Pred. No. 7.4e-107;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTATGATGCTAAGTTTGGTCCCATCATCGCACTCTCTTTTCTGCTCTT 60
 DB 1 GTTTTATTAGTATGATGCTAAGTTTGGTCCCATCATCGCACTCTCTTTTCTGCTCTT 60

QY 61 GTTCTTTTCTGCTTTTCGAAGCACCACCAATGGTGGAAAGCAGAGTTGCGAAAGG 120
 DB 61 GTTCTTTTCTGCTTTTCGAAGCACCACCAATGGTGGAAAGCAGAGTTGCGAAAGG 120

QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAAGCATGCAAGTATGATGCAATT 180
 DB 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAAGCATGCAAGTATGATGCAATT 180

QY 181 AACCTTGAGAAAGCAGACATGATCTTGCACATATGTTCTCCAGCTCACAAGTGTATC 240
 DB 181 AACCTTGAGAAAGCAGACATGATCTTGCACATATGTTCTCCAGCTCACAAGTGTATC 240

QY 241 TGTACTTTCTGTTAAATTTATCGAAACTCTTTGGTGAATAGTTTTATGTAATTTAC 300
 DB 241 TGTACTTTCTGTTAAATTTATCGAAACTCTTTGGTGAATAGTTTTATGTAATTTAC 300

QY 301 ACAAATAAGTCACTGCTCACTATCCATGATGATTTTAAAGCATGTACAGATATGTTAT 360
 DB 301 ACAAATAAGTCACTGCTCACTATCCATGATGATTTTAAAGCATGTACAGATATGTTAT 360

QY 361 GTTGGTTCGTTATACAAATAAAGTTTATTACCAAAAAA 414
 DB 361 GTTGGTTCGTTATACAAATAAAGTTTATTACCAAAAAA 414

RESULT 5
 US-09-077-948A-45
 Sequence 45, Application US/09077948A
 Patent No. 6605698
 GENERAL INFORMATION:
 APPLICANT: Van Amerongen, Aart
 APPLICANT: Fant, Franky
 APPLICANT: Borremans, Frans
 APPLICANT: De Samblanx, Geneveva
 APPLICANT: Sitjtsma, Lolke
 APPLICANT: Meloen, Robbert
 APPLICANT: Puijk, Wouter
 APPLICANT: Schaaper, Wilhelmus
 APPLICANT: Broekaert, Willem
 APPLICANT: Van Gelder, Wilhelmus
 APPLICANT: Rees, Sarah
 TITLE OF INVENTION: Antifungal Proteins
 FILE REFERENCE: 109846-257(SYN-035)
 CURRENT APPLICATION NUMBER: US/09/077,948A
 CURRENT FILING DATE: 1998-08-07
 PRIOR APPLICATION NUMBER: PCT/GB96/03068
 PRIOR FILING DATE: 1996-12-12
 PRIOR APPLICATION NUMBER: GB 9606552.9
 PRIOR FILING DATE: 1996-03-28
 PRIOR APPLICATION NUMBER: GB 9525455.3
 PRIOR FILING DATE: 1995-12-13
 NUMBER OF SEQ ID NOS: 141
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 45
 LENGTH: 414
 TYPE: DNA
 ORGANISM: Raphanus sativus

US-09-077-948A-45

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Query Match      100.0%; Score 414; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 7.4e-107;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATCATCGCTAAGTTTGGGTCATCATCGCACTCTTTTGGTCTCTT 60
DB 1 GTTTATTAGTATCATCGCTAAGTTTGGGTCATCATCGCACTCTTTTGGTCTCTT 60

QY 61 GTTCTTTTGTCTCTTTCGAAGCACCACCAATGTTGGAAGCAGAGTGTGCGAAGG 120
DB 61 GTTCTTTTGTCTCTTTCGAAGCACCACCAATGTTGGAAGCAGAGTGTGCGAAGG 120

QY 121 CCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACCATGCAAGATCAGTGCATT 180
DB 121 CCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACCATGCAAGATCAGTGCATT 180

QY 181 AACCTTGGAAAGCAGCATGATGTCGAACTATGCTTCCACGCTCACAAGTGTATC 240
DB 181 AACCTTGGAAAGCAGCATGATGTCGAACTATGCTTCCACGCTCACAAGTGTATC 240

QY 241 TGTCTACTTCTCTGTTTATTCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
DB 241 TGTCTACTTCTCTGTTTATTCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300

QY 301 ACAAATAAGTCAGTGCATCATGATGATTTAAGACATGACAGATATGTTAT 360
DB 301 ACAAATAAGTCAGTGCATCATGATGATTTAAGACATGACAGATATGTTAT 360

QY 361 GTTGTCTGGTTATACAAATAAAGTTTATTCACCAAAAAA 414
DB 361 GTTGTCTGGTTATACAAATAAAGTTTATTCACCAAAAAA 414

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RESULT 6

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US-08-377-687-58
; Sequence 58, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000

```

TELEFAX: 202-822-0944

```

; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..282
US-08-377-687-58

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```

Query Match      61.4%; Score 254.2; DB 1; Length 288;
Best Local Similarity 98.8%; Pred. No. 3.9e-62;
Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTTATTAGTATCATCGCTAAGTTTGGGTCATCATCGCACTCTTTTGGTCTCTT 60
DB 28 GTTTATTAGTATCATCGCTAAGTTTGGGTCATCATCGCACTCTTTTGGTCTCTT 87

QY 61 GTTCTTTTGTCTCTTTCGAAGCACCACCAATGTTGGAAGCAGAGTGTGCGAAGG 120
DB 88 GTTCTTTTGTCTCTTTCGAAGCACCACCAATGTTGGAAGCAGAGTGTGCGAAGG 147

QY 121 CCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACCATGCAAGATCAGTGCATT 180
DB 148 CCAAGTGGACATGTCAGGAGTCTGTGGAACAATAACCATGCAAGATCAGTGCATT 207

QY 181 AACCTTGGAAAGCAGCATGATGTCGAACTATGCTTCCACGCTCACAAGTGTATC 240
DB 208 AGACTTGGAAAGCAGCATGATGTCGAACTATGCTTCCACGCTCACAAGTGTATC 267

QY 241 TGTCTACTTCTCTGTTTATTCGCAAACTCTTTGGTGAATAGTTTATGTAAT 259
DB 268 TGTCTACTTCTCTGTTTATTCGCAAACTCTTTGGTGAATAGTTTATGTAAT 286

```

RESULT 7

```

US-08-777-192-58
; Sequence 58, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,192
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773

```

REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-861-3000
 TELEFAX: 202-822-0944
 INFORMATION FOR SEQ ID NO: 58:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 288 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: cdna
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 43..282
 US-08-777-192-58

Query Match 61.4%; Score 254.2; DB 1; Length 288;
 Best Local Similarity 98.8%; Pred. No. 3.9e-62;
 Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 60
 Db GTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 87
 QY 61 GTTCTTTTGTGCTTTCGAGACCAACAATGTTGGAAGCAGAGTTTGTCCGAAGG 120
 Db GTTCTTTTGTGCTTTCGAGACCAACAATGTTGGAAGCAGAGTTTGTCCGAAGG 147
 QY 121 CCAAGTGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180
 Db CCAAGTGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 207
 QY 181 AACCTTGAGAAAGCAGACATGATCTTGGAACTATGCTTCCAGCTCACAAAGTGTATC 240
 Db AGACTTGAGAAAGCAGACATGATCTTGGAACTATGCTTCCAGCTCACAAAGTGTATC 267
 QY 241 TGCTACTTTCCTTGTAAAT 259
 Db TGCTACTTTCCTTGTAAAT 286

RESULT 8
 US-08-971-982-58
 Sequence 58, Application US/08971982
 Patent No. 6187904
 GENERAL INFORMATION:
 APPLICANT: BROKABERT, WILLEM F.
 CAMMUE, BRUNO P.A.
 OSBORN, RUPERT W.
 REES, SARAH B.
 TERRAS, FRANKY R.G.
 VANDERLEYDEN, JOZEF
 TITLE OF INVENTION: BIOCIDAL PROTEINS
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CUSHMAN DAREY & CUSHMAN
 STREET: 1100 NEW YORK AVENUE, N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/971,982
 FILING DATE: 17-No. 6187904-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/002,480
 FILING DATE: 04-JAN-1993

ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, PAUL N.
 REGISTRATION NUMBER: 16,773
 REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-861-3000
 TELEFAX: 202-822-0944
 INFORMATION FOR SEQ ID NO: 58:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 288 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: cdna
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 43..282
 SEQUENCE DESCRIPTION: SEQ ID NO: 58:
 US-08-971-982-58
 Query Match 61.4%; Score 254.2; DB 3; Length 288;
 Best Local Similarity 98.8%; Pred. No. 3.9e-62;
 Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 60
 Db GTTTATTAGTATGATGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 87
 QY 61 GTTCTTTTGTGCTTTCGAGACCAACAATGTTGGAAGCAGAGTTTGTCCGAAGG 120
 Db GTTCTTTTGTGCTTTCGAGACCAACAATGTTGGAAGCAGAGTTTGTCCGAAGG 147
 QY 121 CCAAGTGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180
 Db CCAAGTGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 207
 QY 181 AACCTTGAGAAAGCAGACATGATCTTGGAACTATGCTTCCAGCTCACAAAGTGTATC 240
 Db AGACTTGAGAAAGCAGACATGATCTTGGAACTATGCTTCCAGCTCACAAAGTGTATC 267
 QY 241 TGCTACTTTCCTTGTAAAT 259
 Db TGCTACTTTCCTTGTAAAT 286
 RESULT 9
 US-08-627-706-16
 Sequence 16, Application US/08627706
 Patent No. 5773696
 GENERAL INFORMATION:
 APPLICANT: Liang, Jihong
 APPLICANT: Shah, Dilip M.
 APPLICANT: Wu, Yonnie S.
 APPLICANT: Rosenberger, Cindy A.
 TITLE OF INVENTION: Antifungal Polypeptide and Methods for
 Controlling Plant Pathogenic Fungi
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
 STREET: 700 Chesterfield Village Parkway No. 5773696th
 CITY: St. Louis
 STATE: Missouri
 COUNTRY: USA
 ZIP: 63198
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/627,706
 FILING DATE:
 CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELEPHONE: (314)537-6224
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-08-627-706-16

Query Match 52.9%; Score 219; DB 1; Length 285;
Best Local Similarity 90.3%; Pred. No. 2.8e-52;
Matches 234; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 GTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCACTCTCTTTTGGCTGCTCTT 60
Db 16 GTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCACTCTCTTTTGGCTGCTCTC 75
QY 61 GTCTCTTTTGGCTCTTTCGAGGACCAACAATGTTGGTGAAGCAGAGAGTTTGGCGAAGG 120
Db 76 GTCTCTTTTGGCTCTTTCGAGGACCAACAATGTTGGTGAAGCAGAGAGTTTGGCGAAGG 135
QY 121 CCAAGTGGGACATGCTCAGGAGTCTGTGGAACCAATAACCGCATGCAAGAAATCAGTGCATT 180
Db 136 CCATCAGGAGCTTGTCTCAGGAGTCTGTGGAACCAACAACCGCATGCAAGAAATCAGTGCATT 195
QY 181 AACCTTGAGAAAGCAGCAGTATGTTGCAACTATGTTCTCCAGCTCACAAGTGTATC 240
Db 196 AACCTTGAGAAAGCAGCAGTATGTTGCAACTATGTTCTCCAGCTCACAAGTGTATC 255
QY 241 TGCTACTTTCCTTGTAAAT 259
Db 256 TGCTACTTTCCTTGTAAAT 274

RESULT 10

US-09-103-489-16
Sequence 16, Application US/09103489
Patent No. 6215048
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
CONTROLLING PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, B84F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-09-103-489-16

Query Match 52.9%; Score 219; DB 3; Length 285;
Best Local Similarity 90.3%; Pred. No. 2.8e-52;
Matches 234; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 GTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCACTCTCTTTTGGCTGCTCTT 60
Db 16 GTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCACTCTCTTTTGGCTGCTCTC 75
QY 61 GTCTCTTTTGGCTCTTTCGAGGACCAACAATGTTGGTGAAGCAGAGAGTTTGGCGAAGG 120
Db 76 GTCTCTTTTGGCTCTTTCGAGGACCAACAATGTTGGTGAAGCAGAGAGTTTGGCGAAGG 135
QY 121 CCAAGTGGGACATGCTCAGGAGTCTGTGGAACCAATAACCGCATGCAAGAAATCAGTGCATT 180
Db 136 CCATCAGGAGCTTGTCTCAGGAGTCTGTGGAACCAACAACCGCATGCAAGAAATCAGTGCATT 195
QY 181 AACCTTGAGAAAGCAGCAGTATGTTGCAACTATGTTCTCCAGCTCACAAGTGTATC 240
Db 196 AACCTTGAGAAAGCAGCAGTATGTTGCAACTATGTTCTCCAGCTCACAAGTGTATC 255
QY 241 TGCTACTTTCCTTGTAAAT 259
Db 256 TGCTACTTTCCTTGTAAAT 274

RESULT 11

US-09-829-381D-16
Sequence 16, Application US/09829381D
Patent No. 6653280
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
CONTROLLING PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, B84F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381D
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565

Query Match 52.9%; Score 219; DB 4; Length 285;
Best Local Similarity 90.3%; Pred. No. 2.8e-52;
Matches 234; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 GTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCACTCTCTTTTGGCTGCTCTT 60
Db 16 GTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCACTCTCTTTTGGCTGCTCTC 75

QY 61 GTTCTTTTGTGCTTTTCCAAAGCACCACCAATGTTGGAAGCAGACAGAAATTTGTGCAAGG 120
DB 76 GTTCTTTTGTGCTTTTCCGAGCACCACCAATGTTGGAAGCAGACAGAAATTTGTGCAAGG 135
QY 121 CCAAGTGGGATGTCAGGAGTCTGTGGAAACAAATACGATGCAAGATCAGTGCATT 180
DB 136 CCATCAGGAGTCTGTGAGGAGTCTGCGGAAACAAACGATGCAAGATCAGTGCATT 195
QY 181 AACCTTGAGAAAGCAGACATGATCTTTCGAATCTTCCAGCTCACAAGTGTATC 240
DB 196 AACCTGAGAGGACGCGATGATCTTTCGAATCTTCCAGCTCACAAGTGTATC 255
QY 241 TGCTACTTTCTTGTAAAT 259
DB 256 TGCTACTTTCTGCTAAAT 274

RESULT 12

US-08-627-706-17
; Sequence 17, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"

US-08-627-706-17
Query Match 52.1%; Score 215.8; DB 1; Length 285;
Best Local Similarity 89.6%; Pred. No. 2.2e-51;
Matches 232; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 1 GTTTATTAGTATGCTTAAGTTTGGTCCATCATCGCACTCTTTTGTGCTCTT 60
DB 16 GTTTATTAGTATGCTTAAGTTTGGTCCATCATCGCACTCTTTTGTGCTCTC 75
QY 61 GTTCTTTTGTGCTTTTCCAAAGCACCACCAATGTTGGAAGCAGACAGAAATTTGTGCAAGG 120
DB 76 GTTCTTTTGTGCTTTTCCGAGCACCACCAATGTTGGAAGCAGACAGAAATTTGTGCAAGG 135

QY 121 CCAAGTGGGATGTCAGGAGTCTGTGGAAACAAATACGATGCAAGATCAGTGCATT 180
DB 136 CCATCAGGAGTCTGTGAGGAGTCTGCGGAAACAAACGATGCAAGATCAGTGCATT 195
QY 181 AACCTTGAGAAAGCAGACATGATCTTTCGAATCTTCCAGCTCACAAGTGTATC 240
DB 196 AGACTCAGAGGACGCGATGATCTTTCGAATCTTCCAGCTCACAAGTGTATC 255
QY 241 TGCTACTTTCTTGTAAAT 259
DB 256 TGCTACTTTCTGCTAAAT 274

RESULT 13

US-09-103-489-17
; Sequence 17, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,489
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"

US-09-103-489-17
Query Match 52.1%; Score 215.8; DB 3; Length 285;
Best Local Similarity 89.6%; Pred. No. 2.2e-51;
Matches 232; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 1 GTTTATTAGTATGCTTAAGTTTGGTCCATCATCGCACTCTTTTGTGCTCTT 60
DB 16 GTTTATTAGTATGCTTAAGTTTGGTCCATCATCGCACTCTTTTGTGCTCTC 75
QY 61 GTTCTTTTGTGCTTTTCCAAAGCACCACCAATGTTGGAAGCAGACAGAAATTTGTGCAAGG 120
DB 76 GTTCTTTTGTGCTTTTCCGAGCACCACCAATGTTGGAAGCAGACAGAAATTTGTGCAAGG 135
QY 121 CCAAGTGGGATGTCAGGAGTCTGTGGAAACCAATACGATGCAAGATCAGTGCATT 180

Db	136	CCATCAGGACCTTGGTCAGAGCTCTGCGGAACAAACAACGATCGACAGAACCAATGCATC	195
Qy	181	AACCTTGAGAAACACACGACATCGATCTCTTGGCACTATGTCTTCCAGCTCCACAACTGATC	240
Db	136	AGATCTGAGAAGGACCGGATCGATCTTTGCAACTACGCTTCCAGCTCACAAGTGCATC	255
Qy	241	TGCTACTTTCCTTGTTAAT	259
Db	256	TGCTACTTTCCATGCTAAT	274

RESULT 14

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US-09-829-381D-17
; Sequence 17, Application US/09829381D
; Patent No. 6653280
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Controlling Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-829-381D-17

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Query Match 52.1%; Score 215.8; DB 4; Length 285;
Best Local Similarity 89.6%; Pred. No. 2.2e-51;
Matches 232; Conservative 0; Mismatches 27; Indels 0

QY	1	GTTTATTATAGTAGCATCGCTAAGGTTTGCGTCCAATCATCGCACCCTCTTTTGTGCCTCTT	60
Db	16	GTITTTATATAGTAGCATCGCTAAGTITTTGGTTCACATCATCGACTCCTCTTTGTCTCTCTC	75
QY	61	GTTCTTTTGTCTGCTTCCGAAGCAACCAATATGGTGGAAACAAGAAGTTGTGCGAAAGG	120
Db	76	GTTCTCTTTGTCTCTTCGAGCACCAACATATGGTGGAGGCAAAAAGTTGTGCGCAAAGG	135
QY	121	CCAAGTGGGACATGCTCAGGAGTCTGTGGAAACAATAAGCATGCAAGAAATCAGTGCATT	180
Db	136	CCATCAGGGACCTTGGTTCAGGAGTCTGCGGAAACAACAACGCATGCAAGAACCAATGCATC	195
QY	181	AACCTTGAGAAAGCAGCAGCATGGATCTTTGCCAACTATGTCTTCCGAGCTCACAAAGTGTATC	240
Db	196	AGACTCGAAGAGGCACGGCATGGATCTTTGCAACTAAGCTTCCAGCTCACAAAGTGCATC	255
QY	241	TGCTACTTTCTTTGTTTAAT	259
Db	256	TGCTACTTTCCATGCTAAT	274

RESULT 15

US-08-627-706-9
Sequence 9, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Ionnée S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal polypeptide and Methods for
; Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, B84F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO.: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PS-08-627-706-9

Query Match 49.1%; Score 203.4; DB 1; Length 500;
Best Local Similarity 72.5%; Pred. No. 8.4e-48;
Matches 317; Conservative 0; Mismatches 91; Indels 29

[illegible]

Search completed: May 13, 2004, 10:54:47
Job time : 85 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 09:35:52 ; Search time 336 Seconds
(without alignments)
5581.596 Million cell updates/sec

Title:
Perfect score: 414
Sequence: 1 gttttattgatcatggc.....caaaaaaaaaaaaaa 414

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

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Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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19:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	414	100.0	414	9	US-09-759-584-48
2	414	100.0	414	13	US-10-388-361A-45
3	414	100.0	414	14	US-10-006-252A-19
4	254.2	61.4	288	9	US-09-759-584-58
5	242.4	58.6	403	9	US-09-732-561-13
6	223	53.9	400	9	US-09-732-561-15
7	223	53.9	400	9	US-09-887-576-607
8	219	52.9	285	9	US-09-829-381A-16
9	219	52.9	285	13	US-10-681-972-16
10	215.8	52.1	285	9	US-09-829-381A-17
11	215.8	52.1	285	13	US-10-681-972-17
12	203.4	49.1	500	9	US-09-829-381A-9
13	203.4	49.1	500	13	US-10-681-972-9
14	196.6	47.5	243	9	US-09-938-842A-2046

ALIGNMENTS

RESULT 1

US-09-759-584-48

Sequence 48, Application US/09759584

Patent No. US20010014732A1

GENERAL INFORMATION:

APPLICANT: BROEKERT, WILLEM F.

APPLICANT: CAMMUE, BRUNO P.A.

APPLICANT: OSEORN, RUPERT W.

APPLICANT: REES, SARAH B.

APPLICANT: TERRAS, FRANKY R.G.

APPLICANT: VANDERLEIDEN, JOZEF

TITLE OF INVENTION: BIOCIDAL PROTEINS

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DABBY & CUSHMAN

STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/759,584

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/377,687

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..255
US-09-759-584-48

Query Match 100.0%; Score 414; DB 9; Length 414;
Best Local Similarity 100.0%; Pred. No. 3.3e-101;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTATTAGTATCATCGCTAAGTTTGGCGTCCATCATCGCACTTCTTTTGGCTGCTCTT 60
Db 1 GTTTATTAGTATCATCGCTAAGTTTGGCGTCCATCATCGCACTTCTTTTGGCTGCTCTT 60
QY 61 GTTCTTTTGTCTGCTTTCGAAGCACCACCAATGGTGGAGCAGAGAGTTGTGCGAAGG 120
Db 61 GTTCTTTTGTCTGCTTTCGAAGCACCACCAATGGTGGAGCAGAGAGTTGTGCGAAGG 120
QY 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGATGCAAGATCAGTGCATT 180
Db 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGATGCAAGATCAGTGCATT 180
QY 181 AACCTTGAGAAAGCAGCATGATCTTGGCAACTCTTCCAGCTCACAAGTGTATC 240
Db 181 AACCTTGAGAAAGCAGCATGATCTTGGCAACTCTTCCAGCTCACAAGTGTATC 240
QY 241 TGTACTTCTCTTGTATTTATCGCAACTCTTGGTGAATGTTTATGTAATTTAC 300
Db 241 TGTACTTCTCTTGTATTTATCGCAACTCTTGGTGAATGTTTATGTAATTTAC 300
QY 301 ACATAATAGTCAGTGCATCATCCATGAGTATTTTACAGATGTACAGATATGTTAT 360
Db 301 ACATAATAGTCAGTGCATCATCCATGAGTATTTTACAGATGTACAGATATGTTAT 360
QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414
Db 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414

RESULT 2
US-10-388-361A-45
Sequence 45, Application US/10388361A
Publication No. US20030226169A1
GENERAL INFORMATION:
APPLICANT: Van Amerongen, Aart
APPLICANT: Pant, Franky
APPLICANT: Borremans, Frans
APPLICANT: De Samblanx, Genevieve
APPLICANT: Sitjuma, Lolke
APPLICANT: Muelen, Robert
APPLICANT: Puijk, Wouter
APPLICANT: Schaaper, Wilhelms
APPLICANT: Broekaert, Willem
APPLICANT: Van Gelder, Wilhelms
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: 50094PDDIV
CURRENT APPLICATION NUMBER: US/10/388, 361A
CURRENT FILING DATE: 2003-03-13
PRIOR APPLICATION NUMBER: US 09/077,948
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: PCT/GB96/03068
PRIOR FILING DATE: 1996-12-12
PRIOR APPLICATION NUMBER: GB 9606552.9
PRIOR FILING DATE: 1996-03-28

PRIOR APPLICATION NUMBER: GB 9525455.3
PRIOR FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45
LENGTH: 414
TYPE: DNA
ORGANISM: Raphanus sativus
US-10-388-361A-45

Query Match 100.0%; Score 414; DB 13; Length 414;
Best Local Similarity 100.0%; Pred. No. 3.3e-101;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTTATTAGTATCATCGCTAAGTTTGGCGTCCATCATCGCACTTCTTTTGGCTGCTCTT 60
Db 1 GTTTATTAGTATCATCGCTAAGTTTGGCGTCCATCATCGCACTTCTTTTGGCTGCTCTT 60
QY 61 GTTCTTTTGTCTGCTTTCGAAGCACCACCAATGGTGGAGCAGAGAGTTGTGCGAAGG 120
Db 61 GTTCTTTTGTCTGCTTTCGAAGCACCACCAATGGTGGAGCAGAGAGTTGTGCGAAGG 120
QY 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGATGCAAGATCAGTGCATT 180
Db 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGATGCAAGATCAGTGCATT 180
QY 181 AACCTTGAGAAAGCAGCATGATCTTGGCAACTCTTCCAGCTCACAAGTGTATC 240
Db 181 AACCTTGAGAAAGCAGCATGATCTTGGCAACTCTTCCAGCTCACAAGTGTATC 240
QY 241 TGTACTTCTCTTGTATTTATCGCAACTCTTGGTGAATGTTTATGTAATTTAC 300
Db 241 TGTACTTCTCTTGTATTTATCGCAACTCTTGGTGAATGTTTATGTAATTTAC 300
QY 301 ACATAATAGTCAGTGCATCATCCATGAGTATTTTACAGATGTACAGATATGTTAT 360
Db 301 ACATAATAGTCAGTGCATCATCCATGAGTATTTTACAGATGTACAGATATGTTAT 360
QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414
Db 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAA 414

RESULT 3
US-10-006-252A-19
Sequence 19, Application US/10006252A
Publication No. US20020152498A1
GENERAL INFORMATION:
APPLICANT: De Samblanx, Genevieve
APPLICANT: Broekaert, Willem
APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SYN-034DV
CURRENT APPLICATION NUMBER: US/10/006, 252A
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/077,951
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: GB 9525474.4
PRIOR FILING DATE: 1995-12-13
PRIOR APPLICATION NUMBER: PCT/GB96/03065
PRIOR FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 414
TYPE: DNA
ORGANISM: Raphanus sativus
US-10-006-252A-19

Query Match 100.0%; Score 414; DB 14; Length 414;
Best Local Similarity 100.0%; Pred. No. 3.3e-101;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTTTTATAGTATCATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 60
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QY 61 GTTCTTTTGTCTGTTTTCGAAGCACCAACAATGGTGAAGCAGAGAGTTGTGCGAAGG 120
Db 61 GTTCTTTTGTCTGTTTTCGAAGCACCAACAATGGTGAAGCAGAGAGTTGTGCGAAGG 120
QY 121 CCAAGTGGACATGGTCAAGAGTCTGTGGAACAATAACCATGCAAGATCAGTGCATT 180
Db 121 CCAAGTGGACATGGTCAAGAGTCTGTGGAACAATAACCATGCAAGATCAGTGCATT 180
QY 181 AACCTTGAGAAAGCACGACATGGATCTTGCACATGCTTCCAGCTCACAGTGTATC 240
Db 181 AACCTTGAGAAAGCACGACATGGATCTTGCACATGCTTCCAGCTCACAGTGTATC 240
QY 241 TGCTACTTCTGTTAATTAATCGCAAACTCTTGGTGAATAGTTTATGTAATTAC 300
Db 241 TGCTACTTCTGTTAATTAATCGCAAACTCTTGGTGAATAGTTTATGTAATTAC 300
QY 301 ACAAATAAGTCACTGTCATATCCATGAGTGAATTTAGACATGTACAGATATGTTAT 360
Db 301 ACAAATAAGTCACTGTCATATCCATGAGTGAATTTAGACATGTACAGATATGTTAT 360
QY 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414
Db 361 GTTGGTTCGGTTATACAAATAAAGTTTATTCACCAAAAAAATAAAAAA 414
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RESULT 4

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US-09-759-584-58
; Sequence 58, Application US/09759584
; Patent No. US20010014732A1
; GENERAL INFORMATION:
; APPLICANT: BROEKERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERPES, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBAY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,584
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/377,687
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..282
US-09-759-584-58
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Query Match 61.4%; Score 254.2; DB 9; Length 288;
Best Local Similarity 98.8%; Pred. No. 2.8e-58;
Matches 256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 GTTTTATAGTATCATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 60
Db 28 GTTTTATAGTATCATGGCTAAGTTTGGTCCATCATCGCACTTCTTTTGTGCTCTT 87
QY 61 GTTCTTTTGTCTGTTTTCGAAGCACCAACAATGGTGAAGCAGAGAGTTGTGCGAAGG 120
Db 88 GTTCTTTTGTCTGTTTTCGAAGCACCAACAATGGTGAAGCAGAGAGTTGTGCGAAGG 147
QY 121 CCAAGTGGACATGGTCAAGAGTCTGTGGAACAATAACCATGCAAGATCAGTGCATT 180
Db 148 CCAAGTGGACATGGTCAAGAGTCTGTGGAACAATAACCATGCAAGATCAGTGCATT 207
QY 181 AACCTTGAGAAAGCACGACATGGATCTTGCACATGCTTCCAGCTCACAGTGTATC 240
Db 208 AGACTTGAGAAAGCACGACATGGATCTTGCACATGCTTCCAGCTCACAGTGTATC 267
QY 241 TGCTACTTCTGTTAAT 259
Db 268 TGCTACTTCTGTTAAT 286
```

RESULT 5

```
US-09-732-561-13
; Sequence 13, Application US/09732561
; Patent No. US20020035738A1
; GENERAL INFORMATION:
; APPLICANT: Thoma, Bart
; APPLICANT: Terras, Franky
; APPLICANT: Penninckx, Iris
; APPLICANT: Manners, John
; APPLICANT: Kazan, Kemal
; APPLICANT: Broekaert, Willem
; TITLE OF INVENTION: Plant Protection Method
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA AG Products
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/202,638
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/01672
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: PPD 50165/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
```

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE: PD
STRAIN: PDF 1.1
US-09-732-561-13

Query Match 58.6%; Score 242.4; DB 9; Length 403;
Best Local Similarity 76.5%; Pred. No. 5e-55;
Matches 297; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY 1 GTTTTATAGTATCATGCTTAAGTTTGGTCCATCATCGGACATCTCTTTTGGTCTCTTT 60
DB 11 GTATAACAATAGTATGCTTAAGTCTGCTACCATCTTACTCTTTTCTTCTGCTCTTT 70
QY 61 GTCTTTTGGTCTTTCGAGCACCAACATGTTGGAAGCACAGAAAGTTTGTCCGAAAGG 120
DB 71 GTTCTTTTGGTCTTTCGAGCACCAACATGTTGGAAGCACAGAAAGTTTGTCCGAGG 130
QY 121 CCAAGTGGACATGTCAGGAGTCTGTGGAACAAATTAACCATGCAAGATCAGTGCATT 180
DB 131 CCAAGTGGACATGTCGCGAGTTTGGCGAAACAGTAACCGTGCAGAAATCAGTGCATT 190
QY 181 AACCTTGAAAGACGACATGATGTTGCAACTATCTCTCCAGCTCACAGTGTATC 240
DB 191 AACCTTGAAAGACGACATGATGTTGCAACTATCTCTCCAGCTCACAGTGTATC 250
QY 241 TGCTACTTTCCTTTGTAATTTATCGCAACTCTTTTGGTGAATAGTTTATGTAATTTAC 300
DB 251 TGCTACTTTCCTTTGTAATTTATCGCAACTCTTTTGGTGAATAGTTTATGTAATTTAC 310
QY 301 ACAATAAGTACGTCACATCCATGATGTTTAAAGACATGACAGATGTTAT 360
DB 311 CTATTAAATAGTATGTTCTACTCTATGAGAGGCTTATGACATGACAGATGTTAT 370
QY 361 GTTGTTCGGTTATACAAATAAGTTT 388
DB 371 GTTGTTCGGTTATACAAATAAGTTT 398

RESULT 6
US-09-732-561-15
Sequence 15, Application US/09732561
Patent No. US2002035738A1
GENERAL INFORMATION:
APPLICANT: Thomas, Bart
APPLICANT: Terras, Franky
APPLICANT: Penninx, Iris
APPLICANT: Manners, John
APPLICANT: Kazan, Kemal
APPLICANT: Broekaert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSES: ZENECA Ag Products
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732.561
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
STRAIN: PDF1.2
US-09-732-561-15

Query Match 53.9%; Score 223; DB 9; Length 400;
Best Local Similarity 79.9%; Pred. No. 8.2e-50;
Matches 274; Conservative 0; Mismatches 67; Indels 2; Gaps 1;
QY 5 TATTAGTATGATGCTTAAGTTTGGTCCATCATCGGACATCTCTTTTGGTCTCTTTTC 64
DB 21 TATTATATCATGCTTAAGTTTGGTCCATCATCACCTTATCTTCGCTCTCTTTGTTTC 80
QY 65 TTTTGTCTGCTTTCGAGCACCAACAAATGTTGGAAGCACAGAAAGTTTGTCCGAAAGCCAA 124
DB 81 TCTTTGCTGCTTTCGAGCACCAACAAATGTTGGAAGCACAGAAAGTTTGTCCGAGAGCCAA 140
QY 125 GTGGACATGTCAGGAGTCTGTGGAACAAATTAACCATGCAAGATGTCAGATTAACC 184
DB 141 GTGGACATGTCAGGAGTCTGTGGAACAAATTAACCATGCAAGATGTCAGATTAACC 200
QY 185 TTGAGAAAGCACGACATGATCTTCCAACTATGTTTCCAGCTCACAAGTGTATCTGT 244
DB 201 TTGAAGGAGCCCAACATGATCATGCAACTATGTTTCCAGCACACAGTGTATCTGTT 260
QY 245 ACTTTCCTTTGTTAATTTATCGAAACTCTTTGGTGAATAGTTTATGTAATTTACCAA 304
DB 261 ACGTCCCATGTTAAATCTTACCCTAAATCTTTGGTGTAAATCGTGTATTTTACATAAA 320
QY 305 AATAAGTCAAGTCTCACTATCCATGATGATTTTAAAGACATGTA 347
DB 321 AATAAGTCAAGTCTCACTATCCATGATGATTTTAAAGACATGTA 361

RESULT 7
US-09-887-576-607
Sequence 607, Application US/09887576
Patent No. US20020144047A1
GENERAL INFORMATION:
APPLICANT: Budworth, P.
APPLICANT: Brown, D.
APPLICANT: Chang, H.
APPLICANT: Zhu, T.
APPLICANT: Han, B.
APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REFERENCE: 1360.001US1
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/258,692

; PRIOR FILING DATE: 2000-12-29
 ; NUMBER OF SEQ ID NOS: 875
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 607
 ; LENGTH: 400
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(400)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-887-576-607

Query Match 53.9%; Score 223; DB 9; Length 400;
 Best Local Similarity 79.9%; Pred. No. 8.2e-50;
 Matches 274; Conservative 0; Mismatches 67; Indels 2; Gaps 1;
 QY 5 TATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCATTCTTTTGGTCTGTGTTTC 64
 Db 21 TAATAATCATCATGGCTAAGTTTGGCTCCATCATCGCATTCTTTTGGTCTGTGTTTC 80
 QY 65 TTTTGTGCTTTTGAAGCACCACCAATGTTGGAAGCACAAGAGTTGTGCGAAAGCCAA 124
 Db 81 TCATTGTGCTTTTCGACGCCCGGCAATGTTGGAAGCACAAGAGTTGTGCGAAAGCCAA 140
 QY 125 GTGGGACATGTCAGGAGTCTGTGGAACCAATAAGCATGCAAGATCATGATTAACC 184
 Db 141 GTGGGACATGTCAGGAGTCTGTGGAACCAATAAGCATGCAAGATCATGATTAACC 200
 QY 185 TTGAGAAGCAGCATGATGATGTTGCAACTATGTTCCAGCTCAAGTGTATGCT 244
 Db 201 TTGAAGGAGCCAAACATGATGATGTTCCAGCTCAAGTGTATGCT 260
 QY 245 ACTTTCCTGTTAATTATCGCAACTCTTTGGTGAATGTTTATGTAATTACACAA 304
 Db 261 ACGTCCCATGTTAATCTACCACTAATCTTTGGTGTAAATCGTGTATTTACATAAA 320
 QY 305 AATAAGTCAGTGTCACTATCATGAGTGAATTTTAAGACATGTA 347
 Db 321 AATAAGTCAGTGTCACTATCATGAGTGAATTTTAAGACATGTA 361

RESULT 8
 US-09-829-381A-16
 ; Sequence 16, Application US/09829381A
 ; Patent No. US20020144306A1
 ; GENERAL INFORMATION:

APPLICANT: Liang, Jihong
 Shah, Dilip M.
 Wu, Yennie S.
 TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Charles E. Cohen, Monsanto Company, B84F
 STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
 CITY: St. Louis
 STATE: Missouri
 COUNTRY: USA
 ZIP: 63198
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/829,381A
 FILING DATE: 09-Apr-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/103,489
 FILING DATE: 1998-06-24

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cohen, Charles E.
 ; REGISTRATION NUMBER: 34,565
 ; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (314) 537-6224
 ; TELEFAX: (314) 537-6047
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 285 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "synthetic DNA"
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-09-829-381A-16

Query Match 52.9%; Score 219; DB 9; Length 285;
 Best Local Similarity 90.3%; Pred. No. 8.2e-49;
 Matches 234; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
 QY 1 GTTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCATTCTTTTGGTCTGTTC 60
 Db 16 GTTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCATTCTTTTGGTCTGTTC 75
 QY 61 GTTCTTTTCTGCTTTTCGAAGCACCACCAATGTTGGAAGCACAAGTGTGCGAAAGG 120
 Db 76 GTTCTTTTCTGCTTTTCGAAGCACCACCAATGTTGGAAGCACAAGTGTGCGAAAGG 135
 QY 121 CCAAGTGGGACATGTCAGGAGTCTGTGGAACCAATAAGCATGCAAGATCATGTCATT 180
 Db 136 CCATCAGGACTTGGTCAGGAGTCTGCGAAGCACAAGTGTGCGAAGTGTGTCATC 195
 QY 181 AACCTTGAGAAACACGACATGATCTTCCAACTATGTTCTCCAGCTCAAGTGTATC 240
 Db 196 AACCTTGAGAAACACGACATGATCTTCCAACTATGTTCTCCAGCTCAAGTGTATC 255
 QY 241 TGTACTTTTCTGTTTAAT 259
 Db 256 TGTACTTTTCTGTTTAAT 274

RESULT 9
 US-10-681-972-16
 ; Sequence 16, Application US/10681972
 ; Publication No. US20040064850A1
 ; GENERAL INFORMATION:

APPLICANT: Liang, Jihong
 Shah, Dilip M.
 Wu, Yennie S.
 APPLICANT: Rosenberger, Cindy A.
 TITLE OF INVENTION: Antifungal Polypeptide ALTAFF from Alyssum and Methods for Co
 TITLE OF INVENTION: Plant Pathogenic Fungi
 FILE REFERENCE: 38-21 (10700) C
 CURRENT APPLICATION NUMBER: US/10/681,972
 CURRENT FILING DATE: 2003-10-09
 PRIOR APPLICATION NUMBER: US/09/829,381D
 PRIOR FILING DATE: 2001-04-09
 PRIOR APPLICATION NUMBER: 09/103,489
 PRIOR FILING DATE: 1998-06-24
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: Patent in version 3.1
 SEQ ID NO 16
 LENGTH: 285
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic
 US-10-681-972-16
 Query Match 52.9%; Score 219; DB 13; Length 285;
 Best Local Similarity 90.3%; Pred. No. 8.2e-49;

Matches	234;	Conservative	0;	Mismatches	25;	Indels	0;	Gaps	0;
Qy	1	GTTTATTAGTGATCATGGCTAAGTTTGGCTGCCATCATCGCACTCTTTTGTGCTCTT	60						
Db	16	GTTTATTAGTGATCATGGCTAAGTTTGGCTGCCATCATCGCACTCTTTGTGCTCTC	75						
Qy	61	GTTCTTTTGTGCTTTTCGAAGCACCAACAATGTTGGAAGCACAGAAAGTTTGGCGAAAGG	120						
Db	76	GTTCTCTTTGTGCTTTTCGAGGCACCAACTATGTTGGAGGCACAAAGTTTGCAGAGG	135						
Qy	121	CCAAAGTGGGACATGTCAGGAGTGCTGTGGAAAAACAATAACGCATGCAAGAAATCAGTGCATT	180						
Db	136	CCATCAGGGACATTGCTCAGGAGTCTGCGGAAAAACAACGCATGCAAGAACCAATGCAATC	195						
Qy	181	AACCTTGAGAAAGCAGCATCGGATCTTTGCAACTATGCTTCCAGCTCACAAGTGTATC	240						
Db	196	AACCTCGAAGGCACGGCATGGATCTTTGCAACTAGCTCTTCCAGCTCACAAGTGCATC	255						
Qy	241	TGCTACTTTCTTGTGTTAAT	259						
Db	256	TGCTACTTTCCATGCTAAT	274						

RESULT 10
US-09-829-381A-17
; Sequence 17, Application US/09829381A
; Patent No. US2002014306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shan, Dlip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Altha
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-829-381A-17

Best Local Similarity 89.6%; Pred. No. 5.9e-48;
Matches 232; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy	1	GTGTTATTAGTGAATCATGGCTAAGTTTGGTGCCATCATCGCACTTCCTTTTGGCTGCTCTT	60
Db	16	GTGTTATTAGTGAATCATGGCTAAGTTTGGTGCCATCATCGCACTCCCTCTTTTGGCTGCTCTC	75
Qy	61	GTGCTTTTTTGGCTTTCGAAAGCACCAACAATGGTGGAGCACAGAACTTGTGCGAAAGG	120
Db	76	GTGCTTTTTTGGCTTTCGAGGSCACCAACTATGGTGGAGGACCAAAAGTTGTGCCAAAGG	135
Qy	121	CCAAGTGGGACATGGTCAAGAGTCTGTGGAACAATAACGATGCAAGAAATCAAGTCATT	180
Db	136	CCATCAGGGACTTGGTCAAGAGTCTGCGAACAACAACGCGATGCAAGAACCAATGCATC	195
Qy	181	AACCTTGAGAAACGACGACATGGATCTTGCACACTATGCTTCCAGCTCACAAGTGTATC	240
Db	196	AGACTCGAAGGACGCGCATGGAATCTTGCACTACGCTTCCAGCTCACAAGTGCATC	255
Qy	241	TGCTACTTTTCCCTTGTTAAT	259
Db	256	TGCTACTTTCCATGCTAAT	274

RESULT 11
US-10-681-972-17
; Sequence 17, Application US/10681972
; Publication No. US20040064850A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALVAPP from Alyseum and Methods for Control
; TITLE OF INVENTION: Plant Pathogenic Fungi
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/10/681,972
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/829,381D
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-681-972-17

Query Match
52.1%; Score 215.8; DB 9; Length 285;

Db 256 TGCTACTTTCATGCTAAT 274

RESULT 12

US-09-829-381A-9
; Sequence 9, Application US/09829381A
; Patent No. US20020144306A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; ; Shan, Dilip M.
; ; Wu, Yennie S.
; ; Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, B94F
; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,381A
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 500 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-829-381A-9

Query Match 49.1%; Score 203.4; DB 9; Length 500;

Best Local Similarity 72.5%; Pred. No. 1.7e-44;

Matches 317; Conservative 0; Mismatches 91; Indels 29; Gaps 3;

6 ATTAGTATCATGGCTAAGTTTCGCTCCATCATCGCACTTCTTTTGGTCTGTCTTCT 65

59 AGTAATAGATATGGCTAAGTTTCGCTCCATCATCGCACTTCTTTTGGTCTGTCTTCT 118

66 TTTTGTCTGCTTTCGAAGCACCACCAATGTTGGAAACACAGAGTTGTGCGAAGCCCAAG 125

119 CTTTGTCTGCTTTCGAAGCACCACCAATGTTGGAAACACAGAGTTGTGCGAAGCCCAAG 178

126 TGGACATGTCAGGAGTCTGTGGAAACCAATGTTGGAAACCAATGTTGGAAACCAATGTT 185

179 TGAACATGTCAGGAGTCTGTGGAAACCAATGTTGGAAACCAATGTTGGAAACCAATGTT 238

186 TGGAAGCAGCAGCATGGAATCTTCCAGTATGCTTCCAGTATGCTTCCAGTATGCTTCCAGT 245

239 TGAAGAGCAGAACCGGATCTTGAACATGCTTCCAGTATGCTTCCAGTATGCTTCCAGT 298

246 CTTTCTCTTGTAAATTTATCGCAAACTCTTTGGTG-----AATAGTTTTT 289

Db 299 CTTCCCATGTTAATCTACCAATCACTTTTGGTGTGTGTGTATTTTACATGTATG 358

QY 290 ATGTAATTTACACAAATAAGTCAGTCTCACTATCAATGAGTGATTTTAAAGACATGTACC 349

Db 359 TGTTTATTTACATGAATAAGTCTGTGTCA-TCCTTATGGGTGACCTTATGACATGTACC 417

QY 350 AGATATGTTAT-----GTTGGTTCGGTTATACAAATAAAGTTTATTTCACCAA 397

Db 418 AGATATATCATATATGTTGTTTGTGTGTGCGAATTATAACITTTATTTTGTGA 477

QY 398 AAAAAAAAAAAAAAAAAA 414

Db 478 TGCAAAAAAAAAAAAAAA 494

RESULT 13

US-10-681-972-9

; Sequence 9, Application US/10681972

; Publication No. US20040064850A1

; GENERAL INFORMATION:

; APPLICANT: Liang, Jihong

; APPLICANT: Shah, Dilip M.

; APPLICANT: Wu, Yennie S.

; APPLICANT: Rosenberger, Cindy A.

; TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alysum and Methods for Co

; TITLE OF INVENTION: Plant Pathogenic Fungi

; FILE REFERENCE: 38-21 (10700) C

; CURRENT APPLICATION NUMBER: US/10/681,972

; PRIOR FILING DATE: 2003-10-09

; PRIOR APPLICATION NUMBER: US/09/829,381D

; PRIOR FILING DATE: 2001-04-09

; PRIOR APPLICATION NUMBER: 09/103,489

; PRIOR FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 500

; TYPE: DNA

; ORGANISM: Alysum spp

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (22)-(22)

; OTHER INFORMATION: N = any nucleotide

US-10-681-972-9

Query Match 49.1%; Score 203.4; DB 13; Length 500;

Best Local Similarity 72.5%; Pred. No. 1.7e-44;

Matches 317; Conservative 0; Mismatches 91; Indels 29; Gaps 3;

6 ATTAGTATCATGGCTAAGTTTCGCTCCATCATCGCACTTCTTTTGGTCTGTCTTCT 65

59 AGTAATAGATATGGCTAAGTTTCGCTCCATCATCGCACTTCTTTTGGTCTGTCTTCT 118

66 TTTTGTCTGCTTTCGAAGCACCACCAATGTTGGAAACACAGAGTTGTGCGAAGCCCAAG 125

119 CTTTGTCTGCTTTCGAAGCACCACCAATGTTGGAAACACAGAGTTGTGCGAAGCCCAAG 178

126 TGGACATGTCAGGAGTCTGTGGAAACCAATGTTGGAAACCAATGTTGGAAACCAATGTT 185

179 TGAACATGTCAGGAGTCTGTGGAAACCAATGTTGGAAACCAATGTTGGAAACCAATGTT 238

186 TGGAAGCAGCAGCATGGAATCTTCCAGTATGCTTCCAGTATGCTTCCAGTATGCTTCCAGT 245

239 TGAAGAGCAGAACCGGATCTTGAACATGCTTCCAGTATGCTTCCAGTATGCTTCCAGT 298

246 CTTTCTCTTGTAAATTTATCGCAAACTCTTTGGTG-----AATAGTTTTT 289

299 CTTCCCATGTTAATCTACCAATCACTTTTGGTGTGTGTGTATTTTACATGTATG 358

290 ATGTAATTTACACAAATAAGTCAGTCTCACTATGCCAGTGTGATTTTAAAGACATGTACC 349

359 TGTATTATTACATGAATAAGTCTGTGTCA-TCCTTATGGGTGACCTTATGACATGTACC 417

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 09:24:03 ; Search time 2517 Seconds
(without alignments)
4911.777 Million cell updates/sec

Title: US-10-006-252A-19
Perfect score: 414
Sequence: 1 gttttattgatcatggc.....caaaaaaaaaaaaaaaaaaa 414

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 3: em_estin.*
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- 5: em_estov.*
- 6: em_estpi.*
- 7: em_estro.*
- 8: em_hic.*
- 9: gb_estl.*
- 10: gb_est2.*
- 11: gb_hic.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estom.*
- 17: em_gss_hum.*
- 18: em_gss_inv.*
- 19: em_gss_pln.*
- 20: em_gss_vrt.*
- 21: em_gss_fun.*
- 22: em_gss_mam.*
- 23: em_gss_mus.*
- 24: em_gss_pro.*
- 25: em_gss_rpd.*
- 26: em_gss_phg.*
- 27: em_gss_vrl.*
- 28: gb_gss1.*
- 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	313.8	75.8	458	14	CD834994
2	311.2	75.2	470	14	CD831680
3	311	75.1	446	14	CD834068
4	311	75.1	452	14	CD832071

5	310.6	75.0	519	14	CD835064
6	310	74.9	447	14	CD832592
7	309.4	74.7	408	14	CD833779
8	309.4	74.7	409	14	CD834090
9	309.4	74.7	450	14	CD834611
10	308.6	74.5	438	14	CD831294
11	307	74.2	420	14	CD833944
12	307	74.2	421	14	CD826491
13	307	74.2	422	14	CD833983
14	307	74.2	426	14	CD827413
15	307	74.2	438	14	CD831479
16	307	74.2	553	14	CD831014
17	305.4	73.8	418	14	CD832625
18	305.4	73.8	419	14	CD834168
19	305.4	73.8	421	14	CD833977
20	305.4	73.8	421	14	CD837517
21	303.8	73.4	453	14	CD834008
22	302.2	73.0	421	14	CD831111
23	302.2	73.0	422	14	CD831972
24	302.2	73.0	424	14	CD833048
25	302.2	73.0	480	14	CD828332
26	275.2	66.5	449	14	CD833047
27	288.2	64.8	425	14	CD834852
28	288.2	64.8	523	14	CD833661
29	268.2	64.8	543	14	CD828840
30	268	64.7	473	14	CD834995
31	266.6	64.4	427	14	CD833613
32	266.6	64.4	522	14	CD833938
33	266.6	64.4	543	14	CD830628
34	266.4	64.3	482	14	CD833627
35	265.4	64.1	476	14	CD833784
36	265.4	64.1	476	14	CD834092
37	264.8	64.0	481	14	CD833924
38	263.8	63.7	457	14	CD831226
39	263.8	63.7	457	14	CD831392
40	261.2	63.1	409	14	CD832294
41	260.2	62.9	646	14	CD829429
42	258.4	62.4	448	14	CD837568
43	255.6	61.7	543	14	CD829085
44	253.2	61.2	803	28	BH458392
C 45	242.4	58.6	422	9	AV787956

ALIGNMENTS

RESULT 1
LOCUS CD834994 458 bp mRNA linear EST 10-JUL-2003
DEFINITION BN45.043006F011229 BN45 Brassica napus cDNA clone BN45043006, mRNA sequence.
ACCESSION CD834994
VERSION CD834994.1 GI:32516934
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 458)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
FEATURES
Location/Qualifiers
source 1..458

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

Location/Qualifiers

source 1..458

Query Match 75.1%; Score 311; DB 14; Length 446;
Best Local Similarity 89.2%; Pred. No. 2.5e-41;
Matches 347; Conservative 0; Mismatches 40; Indels 2; Gaps 1;

Qy 1 GTTTTATTAGTATGATCGCTAAGTTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTT 60
Db 51 GTATTACTAGTGAGCATGCTAAGTTTGGTCCATCATTTGCCCACTTTTGGCTGCTCTT 110

Qy 61 GTTCTTTTTCGCTCTTTCGAAGCACCACCAATCGTGAAGACAGAAAGTTGCGAAAGG 120
Db 111 GTTCTTTTTCGCTCTTTCGAAGCACCACCAATCGTGAAGACAGAAAGTTGCGAGAGG 170

Qy 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180
Db 171 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 230

Qy 181 AACCTTGAGAAACAGACATGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 240
Db 231 AACCTTGAGAAACAGACATGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 290

Qy 241 TGTACTTCTCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
Db 291 TGTACTTCTCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 350

Qy 301 ACAAATAAGTCTAGTCTACTATCCATGATGATTTTAAAGTGTATC 358
Db 351 ACAAATAAGTCTAGTCTACTATCCATGATGATTTTAAAGTGTATC 410

Qy 359 ATGTTGGTTCGGTTATACAAATAAAGTTT 387
Db 411 ATGTTGGTTCGGTTATACAAATAAAGTTT 439

RESULT 4
CD832071
LOCUS CD832071 452 bp mRNA linear EST 10-JUL-2003
DEFINITION BN40.061003F011227 BN40 Brassica napus cDNA clone BN40061003, mRNA sequence.

ACCESSION CD832071
VERSION CD832071.1 GI:32514011
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 452)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

FEATURES
source
Location/Qualifiers
1..452
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40061003"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN
Query Match 75.1%; Score 311; DB 14; Length 452;
Best Local Similarity 89.2%; Pred. No. 2.4e-41;
Matches 347; Conservative 0; Mismatches 40; Indels 2; Gaps 1;

Qy 1 GTTTTATTAGTATGATCGCTAAGTTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTT 60
Db 55 GTATTACTAGTGAGCATGCTAAGTTTGGTCCATCATTTGCCCACTTTTGGCTGCTCTT 114

Qy 61 GTTCTTTTTCGCTCTTTCGAAGCACCACCAATCGTGAAGACAGAAAGTTGCGAAAGG 120
Db 115 GTTCTTTTTCGCTCTTTCGAAGCACCACCAATCGTGAAGACAGAAAGTTGCGAGAGG 174

Qy 121 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 180
Db 175 CCAAGTGGGACATGGTCAGGAGTCTGTGGAACAATAACGCATGCAAGAAATCAGTGCATT 234

Qy 181 AACCTTGAGAAACAGACATGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 240
Db 235 AACCTTGAGAAACAGACATGATCTTGCACATATGCTTCCAGCTCACAAGTGTATC 294

Qy 241 TGTACTTCTCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
Db 295 TGTACTTCTCTTGTAAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 354

Qy 301 ACAAATAAGTCTAGTCTACTATCCATGATGATTTTAAAGTGTATC 358
Db 355 ACAAATAAGTCTAGTCTACTATCCATGATGATTTTAAAGTGTATC 414

Qy 359 ATGTTGGTTCGGTTATACAAATAAAGTTT 387
Db 415 ATGTTGGTTCGGTTATACAAATAAAGTTT 443

RESULT 5
CD835064
LOCUS CD835064 519 bp mRNA linear EST 10-JUL-2003
DEFINITION BN45.044C21F011228 BN45 Brassica napus cDNA clone BN45044C21, mRNA sequence.

ACCESSION CD835064
VERSION CD835064.1 GI:32517004
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 519)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

FEATURES
source
Location/Qualifiers
1..519
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45044C21"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Query Match 75.0%; Score 310.6; DB 14; Length 519;
Best Local Similarity 86.4%; Pred. No. 2.6e-41;
Matches 355; Conservative 0; Mismatches 54; Indels 2; Gaps 1;

Qy 1 GTTTTATTAGTATGATCGCTAAGTTTGGTCCATCATCGCACTTCTTTTGGCTGCTCTT 60
Db 51 GTATTACTAGTGAGCATGCTAAGTTTGGTCCATCATTTGCCCACTTTTGGCTGCTCTT 110

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QY 61 GTTCTTTTCTGCTTTTGAAGCACCACAAATGTTGGAAGCAGAGAAGTGTGCGAAAGG 120
DB 111 GTTCTTTTCTGCTTTTGAAGCACCACAAATGTTGGAAGCAGAGAAGTGTGCGAGAGG 170

QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 180
DB 171 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 230

QY 181 AACCTTGCAGAAAGCAGACATGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATC 240
DB 231 AACCTTGCAGAAAGCAGACATGATCTTGCAACTATGCTTCCAGCTCACAAGTGTAT 290

QY 241 TGTACTCTTCTGTTAAATTTATCGAAACTCTTTGGTGAATGATTTTATGTAATTTAC 300
DB 291 TGTACTCTTCTGTTAAATTTATCGAAACTCTTTGGTGAATGATTTTATGTAATTTAC 350

QY 301 ACAAATAAGTCAGTGCACATCCATGAGTGAATTTTAAGACATGTACC--AGATATGTT 358
DB 351 ATAAATAAGTCAGTGCACATCCATGAGTGAATTTTAAGACATGTACC--AGATATGTT 410

QY 359 ATGTTGGTTCGGTATACAAATAAAGTTTTATTACCAAAAAAATAAAAAA 409
DB 411 ATGTTGGTTCGGTATACAAATAAAGTTTTATTACCAAAAAAATAAAAAA 461

RESULT 6
CD8332592 447 bp mRNA linear EST 10-JUL-2003
LOCUS BN40.063015F011228 BN40 Brassica napus cDNA clone BN40063015, mRNA
DEFINITION sequence.
ACCESSION CD8332592.1 GI:32514532
VERSION CD8332592.1
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 447)
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Unpublished (2003)
JOURNAL Contact: Genoplante
COMMENT Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
source
location/Qualifiers
1..447
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN40063015"
/tissue_type="seed"
/clone_lib="BN40"

ORIGIN
Query Match 74.9%; Score 310; DB 14; Length 447;
Best Local Similarity 88.9%; Pred. No. 3.6e-41;
Matches 346; Conservative 0; Mismatches 41; Indels 2; Gaps 1;

QY 1 GTTTTATTAGTATGATGGCTAAGTTTGGTCCATCATCGCACTTTCTTTTGTGCTCTT 60
DB 50 GTATTACTAGTATGATGGCTAAGTTTGGTCCATCATCGCACTTTCTTTTGTGCTCTT 109

QY 61 GTTCTTTTCTGCTTTTGAAGCACCACAAATGTTGGAAGCAGAGAAGTGTGCGAAAGG 120
DB 110 GTTCTTTTCTGCTTTTGAAGCACCACAAATGTTGGAAGCAGAGAAGTGTGCGAGAGG 169

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QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 180
DB 170 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 229

QY 181 AACCTTGCAGAAAGCAGACATGATCTTGCAACTATGCTTCCAGCTCACAAGTGTATC 240
DB 230 AACCTTGCAGAAAGCAGACATGATCTTGCAACTATGCTTCCAGCTCACAAGTGTAT 289

QY 241 TGTACTCTTCTGTTAAATTTATCGAAACTCTTTGGTGAATGATTTTATGTAATTTAC 300
DB 290 TGTACTCTTCTGTTAAATTTATCGAAACTCTTTGGTGAATGATTTTATGTAATTTAC 349

QY 301 ACAAATAAGTCAGTGCACATCCATGAGTGAATTTTAAGACATGTACC--AGATATGTT 358
DB 350 ATAAATAAGTCAGTGCACATCCATGAGTGAATTTTAAGACATGTACC--AGATATGTT 409

QY 359 ATGTTGGTTCGGTATACAAATAAAGTTTT 387
DB 410 ATGTTGGTTCGGTATACAAATAAAGTTTT 438

RESULT 7
CD833779 408 bp mRNA linear EST 10-JUL-2003
LOCUS BN45.001115F010914 BN45 Brassica napus cDNA clone BN45001115, mRNA
DEFINITION sequence.
ACCESSION CD833779
VERSION CD833779.1 GI:32515719
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 408)
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Unpublished (2003)
JOURNAL Contact: Genoplante
COMMENT Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
source
location/Qualifiers
1..408
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45001115"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Query Match 74.7%; Score 309.4; DB 14; Length 408;
Best Local Similarity 88.9%; Pred. No. 4.8e-41;
Matches 346; Conservative 0; Mismatches 41; Indels 2; Gaps 1;

QY 1 GTTTTATTAGTATGATGGCTAAGTTTGGTCCATCATCGCACTTTCTTTTGTGCTCTT 60
DB 13 GTATTACTAGTATGATGGCTAAGTTTGGTCCATCATCGCACTTTCTTTTGTGCTCTT 72

QY 61 GTTCTTTTCTGCTTTTGAAGCACCACAAATGTTGGAAGCAGAGAAGTGTGCGAAAGG 120
DB 73 GTTCTTTTCTGCTTTTGAAGCACCACAAATGTTGGAAGCAGAGAAGTGTGCGAGAGG 132

QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 180
DB 133 CCAAGTGGGACATGGTCAGAGTCTGTGGAACAATAACGCATGCAAGATCAGTGCATT 192

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QY 181 AACCTTGAGAAAGCAGCATGGATCTTGGCAACTATGCTTCCAGCTCACAAGTGTATC 240
 Db |||||
 QY 193 AACCTTGAGAAAGCAGCATGGATCTTGGCAACTATGCTTCCAGCTCACAAGTGTAT 252
 Db |||||
 QY 241 TGGTACTTCCCTTGTATTTATCGCAACTCTTTGGTGAATAGTATTTTAAATTTAC 300
 Db |||||
 QY 253 TGGTACTTCCCTTGTATTTATCGCAACTCTTTGGTGAATAGTATTTTAAATTTAC 312
 Db |||||
 QY 301 ACAAATAAGTCAGTGCATCTATCCATGAGTGAATTTAAGACATGTACC--AGATATGTT 358
 Db |||||
 QY 313 ATAAATAAGTCTGTGTCATCTATCAATGAGTGAATTTTATGACATGTACCTGATATGTT 372
 Db |||||
 QY 359 ATGTTGGTTCGGTTATCAATAAAGTTT 387
 Db |||||
 QY 373 ATGTTGGTTCGGTTATCAATAAAGTTT 401

RESULT 8
 LOCUS CD834090
 DEFINITION BN45.040212F011018 BN45 Brassica napus cDNA clone BN45040121, mRNA
 sequence.
 ACCESSION CD834090
 VERSION CD834090.1 GI:32516030
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 409)
 AUTHORS Genoplante.
 TITLE Genoplante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>
 and <http://genoplante-info.infobiogen.fr>).
 FEATURES
 source
 1. 409
 Location/Qualifiers
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45040121"
 /tissue_type="seed"
 /clone_lib="BN45"

Query Match 74.7%; Score 309.4; DB 14; Length 409;
 Best Local Similarity 88.9%; Pred. No. 4.7e-41;
 Matches 346; Conservative 0; Mismatches 41; Indels 2; Gaps 1;
 QY 1 GTTTATTAGTATGATGCTAAGTTTGGTCCATCGCATCTTTTGGTCTCTT 60
 Db 14 GTATTACTAGTATGATGCTAAGTTTGGTCCATCGCATCTTTTGGTCTCTT 73
 QY 61 GTTCTTTTGTCTCTTTCGAAGCACCACCAATGTTGGGAAGCAGCAAGTTTGGCAAGG 120
 Db 74 GTTCTTTTGTCTCTTTCGAAGCACCACCAATGTTGGGAAGCAGCAAGTTTGGCAAGG 133
 QY 121 CCAAGTGGGACATGCTCAGAGTCTGTGGAACAATAACGATGCAAGATCAAGTGCATT 180
 Db 134 CCAAGTGGGACATGCTCAGAGTCTGTGGAACAATAACGATGCAAGATCAAGTGCATT 193
 QY 181 AACCTTGAGAAAGCAGCATGATCTTCCAACTATGCTTCCAGCTCACAAGTGTATC 240
 Db 194 AACCTTGAGAAAGCAGCATGATCTTCCAACTATGCTTCCAGCTCACAAGTGTAT 253

QY 241 TGGTACTTCCCTTGTATTTATCGCAACTCTTTGGTGAATAGTATTTTAAATTTAC 300
 Db |||||
 QY 254 TGGTACTTCCCTTGTATTTATCGCAACTCTTTGGTGAATAGTATTTTAAATTTAC 313
 Db |||||
 QY 301 ACAAATAAGTCAGTGCATCTATCCATGAGTGAATTTAAGACATGTACC--AGATATGTT 358
 Db |||||
 QY 314 ATAAATAAGTCTGTGTCATCTATCAATGAGTGAATTTTATGACATGTACCTGATATGTT 373
 Db |||||
 QY 359 ATGTTGGTTCGGTTATCAATAAAGTTT 387
 Db |||||
 QY 374 ATGTTGGTTCGGTTATCAATAAAGTTT 402

RESULT 9
 LOCUS CD834611
 DEFINITION BN45.042H07F011228 BN45 Brassica napus cDNA clone BN45042H07, mRNA
 sequence.
 ACCESSION CD834611
 VERSION CD834611.1 GI:32516551
 KEYWORDS EST.
 SOURCE Brassica napus (rape)
 ORGANISM Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 450)
 AUTHORS Genoplante.
 TITLE Genoplante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>
 and <http://genoplante-info.infobiogen.fr>).
 FEATURES
 source
 1. 450
 Location/Qualifiers
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN45042H07"
 /tissue_type="seed"
 /clone_lib="BN45"

Query Match 74.7%; Score 309.4; DB 14; Length 450;
 Best Local Similarity 88.9%; Pred. No. 4.4e-41;
 Matches 346; Conservative 0; Mismatches 41; Indels 2; Gaps 1;
 QY 1 GTTTATTAGTATGATGCTAAGTTTGGTCCATCGCATCTTTTGGTCTCTT 60
 Db 51 GTATTACTAGTATGATGCTAAGTTTGGTCCATCGCATCTTTTGGTCTCTT 110
 QY 61 GTTCTTTTGTCTCTTTCGAAGCACCACCAATGTTGGGAAGCAGCAAGTTTGGCAAGG 120
 Db 111 GTTCTTTTGTCTCTTTCGAAGCACCACCAATGTTGGGAAGCAGCAAGTTTGGCAAGG 170
 QY 121 CCAAGTGGGACATGCTCAGAGTCTGTGGAACAATAACGATGCAAGATCAAGTGCATT 180
 Db 171 CCAAGTGGGACATGCTCAGAGTCTGTGGAACAATAACGATGCAAGATCAAGTGCATT 230
 QY 181 AACCTTGAGAAAGCAGCATGATCTTCCAACTATGCTTCCAGCTCACAAGTGTATC 240
 Db 231 AACCTTGAGAAAGCAGCATGATCTTCCAACTATGCTTCCAGCTCACAAGTGTAT 290
 QY 241 TGGTACTTCCCTTGTATTTATCGCAACTCTTTGGTGAATAGTATTTTAAATTTAC 300
 Db 291 TGGTACTTCCCTTGTATTTATCGCAACTCTTTGGTGAATAGTATTTTAAATTTAC 350

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QY 301 ACAGTAATAGTCAGTGTCTACTATCCATGAGTGAATTTAAGACATGTACC--AGATATGTT 358
Db |||||
QY 351 ATAAAAAATAGTCTGTGTCTACATCAATGAGTGAATTTATGACATGTACCTGATATATGTT 410
Db |||||
QY 359 ATGTTGGTTTCGGTTATACAAATAAAGTTT 387
Db |||||
QY 411 ATGTTGGTTTCGGTTATATAAATAAAGTTT 439
Db |||||

RESULT 10
CD831294
LOCUS
DEFINITION
  BN40.058N13F011019 BN40 Brassica napus cDNA clone BN40058N13, mRNA
  sequence.
ACCESSION
  CD831294
VERSION
  CD831294.1 GI:32513234
KEYWORDS
  EST.
SOURCE
  Brassica napus (rape)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 438)
  Genoplatte, a major partnership french program in plant genomics
  Unpublished (2003)
  JOURNAL
  CONTACT: Genoplatte
  COMMENT
  93, rue Henri Rochefort 91025 EVRY CEDEX France
  Tel: 33 1 69 47 54 00
  Fax: 33 1 69 47 54 10
  This sequence has been generated in the framework of the french
  plant genomics programme 'Genoplatte' (http://www.genoplatte.com
  and http://genoplatte-info.infobiogen.fr).

FEATURES
  source
  1..438
    location/Qualifiers
    /organism="Brassica napus"
    /mol_type="mRNA"
    /cultivar="Jet neuf"
    /db_xref="taxon:3708"
    /clone="BN40058N13"
    /tissue_type="seed"
    /clone_lib="BN40"

ORIGIN
  Query Match 74.5%; Score 308.6; DB 14; Length 438;
  Best Local Similarity 90.6%; Pred. No. 6.1e-41;
  Matches 329; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTATGATCGCTTAAGTTTGGCTCCATCATCGCACTCTTTTCTGCTCTT 60
Db |||||
QY 36 GTATTACTAGTATGATCGCTTAAGTTTGGCTCCATCATCGCACTCTTTTCTGCTCTT 95
Db |||||
QY 61 GTCTTTTGTCTGCTTTCGAAAGCACCACCAATGCTGGAAGCAGAGTGTGCGAAGG 120
Db |||||
QY 96 GTCCTTTTGTCTGCTTTCGAAAGCACCACCAATGCTGGAAGCAGAGTGTGCGAAGG 155
Db |||||
QY 121 CCAAGTGGGACATGCTGAGGAGTCTGTGGAACAATAACGCATGCAAGTGTGCGAAT 180
Db |||||
QY 156 CCAAGTGGGACATGCTGAGGAGTCTGTGGAACAATAACGCATGCAAGTGTGCGAAT 215
Db |||||
QY 181 AACCTTGAAGAACGACATGGAATCTTGCAACTATGTCTTCCAGCTCACAAGTGTATC 240
Db |||||
QY 216 AACCTTGAAGAACGACATGGAATCTTGCAACTATGTCTTCCAGCTCACAAGTGTAT 275
Db |||||
QY 241 TGCTACTTTCCTTCTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
Db |||||
QY 276 TGCTACTTTCCTTCTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 335
Db |||||
QY 301 ACAGTAATAGTCAGTGTCTACTATCCATGAGTGAATTTAAGACATGTACCATATGTTAT 360
Db |||||
QY 336 ATAAAAAATAGTCTGTGTCTACATCAATGAGTGAATTTATGACATGTACCTGATATGTTAT 395
Db |||||

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QY 361 GTT 363
Db |||||
QY 396 GTT 398
Db |||||

RESULT 11
CD833944
LOCUS
DEFINITION
  BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, mRNA
  sequence.
ACCESSION
  CD833944
VERSION
  CD833944.1 GI:32515884
KEYWORDS
  EST.
SOURCE
  Brassica napus (rape)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 420)
  Genoplatte, a major partnership french program in plant genomics
  Unpublished (2003)
  JOURNAL
  CONTACT: Genoplatte
  COMMENT
  93, rue Henri Rochefort 91025 EVRY CEDEX France
  Tel: 33 1 69 47 54 00
  Fax: 33 1 69 47 54 10
  This sequence has been generated in the framework of the french
  plant genomics programme 'Genoplatte' (http://www.genoplatte.com
  and http://genoplatte-info.infobiogen.fr).

FEATURES
  source
  1..420
    location/Qualifiers
    /organism="Brassica napus"
    /mol_type="mRNA"
    /cultivar="Jet neuf"
    /db_xref="taxon:3708"
    /clone="BN45040B07"
    /tissue_type="seed"
    /clone_lib="BN45"

ORIGIN
  Query Match 74.2%; Score 307; DB 14; Length 420;
  Best Local Similarity 90.4%; Pred. No. 1.1e-40;
  Matches 328; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 GTTTTATTAGTATGATCGCTTAAGTTTGGCTCCATCATCGCACTCTTTTCTGCTCTT 60
Db |||||
QY 35 GTATTACTAGTATGATCGCTTAAGTTTGGCTCCATCATCGCACTCTTTTCTGCTCTT 94
Db |||||
QY 61 GTCTTTTGTCTGCTTTCGAAAGCACCACCAATGCTGGAAGCAGAGTGTGCGAAGG 120
Db |||||
QY 95 GTCCTTTTGTCTGCTTTCGAAAGCACCACCAATGCTGGAAGCAGAGTGTGCGAAGG 154
Db |||||
QY 121 CCAAGTGGGACATGCTGAGGAGTCTGTGGAACAATAACGCATGCAAGTGTGCGAAT 180
Db |||||
QY 155 CCAAGTGGGACATGCTGAGGAGTCTGTGGAACAATAACGCATGCAAGTGTGCGAAT 214
Db |||||
QY 181 AACCTTGAAGAACGACATGGAATCTTGCAACTATGTCTTCCAGCTCACAAGTGTATC 240
Db |||||
QY 215 AACCTTGAAGAACGACATGGAATCTTGCAACTATGTCTTCCAGCTCACAAGTGTAT 274
Db |||||
QY 241 TGCTACTTTCCTTCTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
Db |||||
QY 275 TGCTACTTTCCTTCTGTTAATTTATCGCAAACTCTTTGGTGAATAGTTTATGTAATTTAC 334
Db |||||
QY 301 ACAGTAATAGTCAGTGTCTACTATCCATGAGTGAATTTAAGACATGTACCATATGTTAT 360
Db |||||
QY 335 ATAAAAAATAGTCTGTGTCTACATCAATGAGTGAATTTATGACATGTACCTGATATGTTAT 394
Db |||||
QY 361 GTT 363
Db |||||
QY 395 GTT 397
Db |||||

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RESULT 12
CD826491
LOCUS
DEFINITION
CD826491 421 bp mRNA linear EST 10-JUL-2003
BN25.064A05F020416 BN25 Brassica napus cDNA clone BN25064A05, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CD826491.1 GI:32508431
EST.
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 421)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.inbio.gen.fr>).

FEATURES
source
Location/Qualifiers
1..421
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN25064A05"
/tissue_type="seed"
/clone_lib="BN25"

ORIGIN
Query Match 74.2%; Score 307; DB 14; Length 421;
Best Local Similarity 90.4%; Pred. No. 1.1e-40;
Matches 328; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 1 GTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGTGCTCTT 60
DB 36 GTATTACTAGTATCATGGCTAAGTTTGGCTCCATCATTCGCCCTACTTTTGTGCTCTT 95
QY 61 GTTCTTTTGTGCTTTCGAGCACCAACAATGGTGGAGACACAGAAGTTGCGAAAGG 120
DB 96 GTCTTTTGTGCTCTTCGAGCACCAACAATGGTGGAGACACAGAAGTTGCGAGAGG 155
QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGCAAGTATCAGTGCATT 180
DB 156 CCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGCAAGTATCAGTGCATT 215
QY 181 AACCTTGAGAAAGACACATGATCTTGCACATATGTCTTCCAGCTCACAAGTGTATC 240
DB 216 AACCTTGAGAAAGACACATGATCTTGCACATATGTCTTCCAGCTCACAAGTGTAT 275
QY 241 TGTCTTTTCTTGTAAATTTATCGCAACTCTTTGGTGAATAGTTTTATGTAATTAC 300
DB 276 TGTCTTTCTTGTAACTTATGCGCAAACTCTTTGGTGGTGTAGTTTGTGTAATTAC 335
QY 301 AAAAAAATAGTCACTATCCATGAGTGAATTTTAAGACATGTACCATATGTTAT 360
DB 336 ATAAATAAGTCTGTCTCATCATCAATGAGTGAATTTATGCAATGCTACTGATATGTTAT 395
QY 361 GTT 363
DB 396 GTT 398

RESULT 13
CD833983

LOCUS
DEFINITION
CD833983 422 bp mRNA linear EST 10-JUL-2003
BN45.040D11F011019 BN45 Brassica napus cDNA clone BN45040D11, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CD833983.1 GI:32515923
EST.
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 422)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.inbio.gen.fr>).

FEATURES
source
Location/Qualifiers
1..422
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN45040D11"
/tissue_type="seed"
/clone_lib="BN45"

ORIGIN
Query Match 74.2%; Score 307; DB 14; Length 422;
Best Local Similarity 90.4%; Pred. No. 1.1e-40;
Matches 328; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 1 GTTTATTAGTATCATGGCTAAGTTTGGCTCCATCATCGCACTTCTTTTGTGCTCTT 60
DB 36 GTATTACTAGTATCATGGCTAAGTTTGGCTCCATCATTCGCCCTACTTTTGTGCTCTT 95
QY 61 GTTCTTTTGTGCTTTCGAGCACCAACAATGGTGGAGACACAGAAGTTGCGAAAGG 120
DB 96 GTCTTTTGTGCTCTTCGAGCACCAACAATGGTGGAGACACAGAAGTTGCGAGAGG 155
QY 121 CCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGCAAGTATCAGTGCATT 180
DB 156 CCAAGTGGGACATGGTCAGAGTCTGTGGAAACAATAACGCATGCAAGTATCAGTGCATT 215
QY 181 AACCTTGAGAAAGACACATGATCTTGCACATATGTCTTCCAGCTCACAAGTGTATC 240
DB 216 AACCTTGAGAAAGACACATGATCTTGCACATATGTCTTCCAGCTCACAAGTGTAT 275
QY 241 TGTCTTTTCTTGTAAATTTATCGCAACTCTTTGGTGAATAGTTTTATGTAATTAC 300
DB 276 TGTCTTTCTTGTAACTTATGCGCAAACTCTTTGGTGGTGTAGTTTGTGTAATTAC 335
QY 301 AAAAAAATAGTCACTATCCATGAGTGAATTTTAAGACATGTACCATATGTTAT 360
DB 336 ATAAATAAGTCTGTCTCATCATCAATGAGTGAATTTATGCAATGCTACTGATATGTTAT 395
QY 361 GTT 363
DB 396 GTT 398

RESULT 14
CD827413
LOCUS
DEFINITION
CD827413 426 bp mRNA linear EST 10-JUL-2003
BN25.067G02F020123 BN25 Brassica napus cDNA clone BN25067G02, mRNA
sequence.
ACCESSION
CD827413

VERSION CD827413.1 GI:32509353
 EST.
 KEYWORDS Brassica napus (rape)
 SOURCE
 ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 426)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>
 and <http://genoplante-info.infobiogen.fr>).

FEATURES
 source

1..426
 /organism="Brassica napus"
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 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN25067G02"
 /tissue_type="seed"
 /clone_lib="BN25"

ORIGIN

Query Match 74.2%; Score 307; DB 14; Length 426;
 Best Local Similarity 90.4%; Pred. No. 1.1e-40;
 Matches 328; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATGCGACTTCTTTTGTGCTCTT 60
 Db |||||
 Qy 61 GTTCTTTTGTCTTTTGAAGCACCACCAATGTTGGAGACACAGAGTTGCGAAGG 120
 Db |||||
 Qy 96 GTCTTTTTCGCTCTCGAAGCACCACCAATGTTGGAGACACAGAGTTGTCGAGAG 155
 Db |||||
 Qy 121 CCAAGTGGGACATGTTGAGAGTCTGTGGAACCAATTAACGATGCAAGATCAGTGCATT 180
 Db |||||
 Qy 156 CCAAGTGGGACATGTTGAGAGTCTGTGGAACCAATTAACGATGCAAGATCAGTGCATT 215
 Db |||||
 Qy 181 AACCTTGAGAAAGCAGACATGGAATCTTGCAACTATGTTCTCCAGCTCACAAGTGATC 240
 Db |||||
 Qy 216 AACCTTGAGAAAGCAGACATGGAATCTTGCAACTATGTTCTCCAGCTCACAAGTGATC 275
 Db |||||
 Qy 241 TGTACTTTCCCTTGTAAATTTATCGAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
 Db |||||
 Qy 276 TGTACTTTCCCTTGTAAATTTATCGAAACTCTTTGGTGAATAGTTTATGTAATTTAC 335
 Db |||||
 Qy 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTATTTTAAGACATGTACCATATGTTAT 360
 Db |||||
 Qy 336 ATAAATAAAGTCAGTGTCACTATCCATGAGTATTTTAAGACATGTACCATATGTTAT 395
 Qy 361 GTT 363
 Db 396 GTT 398

RESULT 15

CD831479
 LOCUS
 DEFINITION BN40.059J13F011208 BN40 Brassica napus cDNA clone BN40059J13, mRNA
 sequence.
 ACCESSION CD831479
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 438)

Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>
 and <http://genoplante-info.infobiogen.fr>).

FEATURES
 source

1..438
 /organism="Brassica napus"
 /mol_type="mRNA"
 /cultivar="Jet neuf"
 /db_xref="taxon:3708"
 /clone="BN40059J13"
 /tissue_type="seed"
 /clone_lib="BN40"

ORIGIN

Query Match 74.2%; Score 307; DB 14; Length 438;
 Best Local Similarity 90.4%; Pred. No. 1.1e-40;
 Matches 328; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 GTTTATTAGTATCATGGCTAAGTTTGGTCCATCATGCGACTTCTTTTGTGCTCTT 60
 Db 36 GTATTACTAGTATCATGGCTAAGTTTGGTCTTCCATCATGCGCTTCTTTTGTGCTCTT 95
 Qy 61 GTTCTTTTGTCTCTTGAAGCACCACCAATGTTGGAGACACAGAGTTGTCGAGAGG 120
 Db 96 GTCTTTTTCGCTCTCTGAAGCACCACCAATGTTGGAGACACAGAGTTGTCGAGAGG 155
 Qy 121 CCAAGTGGGACATGTTGAGAGTCTGTGGAACCAATTAACGATGCAAGATCAGTGCATT 180
 Db 156 CCAAGTGGGACATGTTGAGAGTCTGTGGAACCAATTAACGATGCAAGATCAGTGCATT 215
 Qy 181 AACCTTGAGAAAGCAGACATGGAATCTTGCAACTATGTTCTCCAGCTCACAAGTGATC 240
 Db 216 AACCTTGAGAAAGCAGACATGGAATCTTGCAACTATGTTCTCCAGCTCACAAGTGATC 275
 Qy 241 TGTACTTTCCCTTGTAAATTTATCGAAACTCTTTGGTGAATAGTTTATGTAATTTAC 300
 Db 276 TGTACTTTCCCTTGTAAATTTATCGAAACTCTTTGGTGAATAGTTTATGTAATTTAC 335
 Qy 301 ACAAAATAAGTCAGTGTCACTATCCATGAGTATTTTAAGACATGTACCATATGTTAT 360
 Db 336 ATAAATAAAGTCAGTGTCACTATCCATGAGTATTTTAAGACATGTACCATATGTTAT 395
 Qy 361 GTT 363
 Db 396 GTT 398

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 Job time : 2524 secs